



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 116342

TO: Phuong Bui
Location: REM-2A15/2C18
Art Unit: 1638
Wednesday, March 10, 2004

Case Serial Number: 10/033109

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen E01A69
Phone: 571-272-2518

BOB
barbara.obryen@uspto.gov

Search Notes

RUSH

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2004, 10:35:31 ; Search time 6735 Seconds
(without alignments)
10978.948 Million cell updates/sec

Title: US-10-033-109-3

Perfect score: 1706

Sequence: 1 Gcagagcactcccaaccccc.....aaaaaaaaaaaaaaaaaaaaa 1706

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	910.8	53.4	1797	8	AF182188	AF182188 Lotus jap
2	832.8	48.8	1557	8	AV135020	AV135020 Lotus jap
3	768.6	45.1	1991	8	BT009318	BT009318 Triticum
4	755.8	44.3	1506	6	AX412659	AX412659 Sequence
5	755.8	44.3	1506	6	AX508508	AX508508 Sequence
6	755.8	44.3	1700	8	ATAMT1	X75879 A.thaliana
7	755.8	44.3	1748	6	A44314	A44314 Sequence 1
8	755.8	44.3	1748	6	AR399484	AR399484 Sequence
9	755.8	44.3	113970	8	ATT6G15	AL049656 Arabidops
10	755.8	44.3	199634	8	ATCHRIV36	AL161536 Arabidops
11	753.8	44.2	69812	8	AP004059	AP004059 Arabidops
12	752.2	44.1	1853	8	AK107204	AK107204 Oryza sat
13	739.6	43.4	128913	2	AF004053	AF004053 Oryza sat
14	738.2	43.3	2044	8	AK073718	AK073718 Oryza sat
15	738.2	43.3	4123	8	AF289477	AF289477 Oryza sat
16	738.2	43.3	103039	8	OSJUN0068	AF606607 Oryza sat
17	736.2	43.2	1751	8	LEAMT1	X92854 L.esculentu
18	730.4	42.8	1817	8	AK107601	AK107601 Oryza sat
19	723	42.4	2987	8	AF289479	AF289479 Oryza sat
20	720.2	42.2	1706	8	AY037219	AY037219 Arabidops
21	713.8	41.8	224188	2	AC139709	AC139709 Medicago
22	705.8	41.4	1545	6	AX506795	AX506795 Sequence
23	705.8	41.4	1642	8	AY093374	AY093374 Arabidops
24	705.8	41.4	1846	8	AF110771	AF110771 Arabidops
25	705.8	41.4	1847	8	AY062571	AY062571 Arabidops
26	705.8	41.4	118335	8	AC006193	AC006193 Arabidops
27	700.4	41.1	1497	6	AX507192	AX507192 Sequence
28	700.4	41.1	1671	8	AF083035	AF083035 Arabidops
29	700.4	41.1	80393	8	AF000382	AF000382 Arabidops
30	699.4	41.0	1790	8	AF083036	AF083036 Arabidops
31	694	40.7	1731	8	AF306518	AF306518 Brassica
32	672.6	39.4	4654	8	AF289478	AF289478 Oryza sat
33	667.4	39.1	97155	8	ATF16A16	AL035353 Arabidops
34	667.4	39.1	197655	8	ATCHRIV69	AL181573 Arabidops
35	660.6	38.7	1768	8	AK105667	AK105667 Oryza sat
36	660.2	38.7	127431	2	AC146819	AC146819 Medicago
37	635.6	37.3	139089	2	AC146571	AC146571 Medicago
38	635.4	37.2	1858	8	LEAMT2GEN	X95098 L.esculentu
39	632.6	37.1	2046	8	AF001505	AF001505 Oryza sat
40	539.6	31.6	2720	8	LTA279059	AJ279059 Lotus jap
41	527.6	30.9	1004	8	AF080541	AF080541 Nepenthes
42	452.2	26.5	1659	8	AF118858	AF118858 Lycopersi
43	300.2	17.6	555	8	AF188744	AF188744 Brassica
44	298.8	17.5	591	11	AL772895	AL772895 Arabidops
45	265.2	15.5	468	8	AY113167	AY113167 Arabidops

ALIGNMENTS

RESULT 1
AF182188
LOCUS
DEFINITION Lotus japonicus putative ammonium transporter AMT1.1 mRNA, complete cds.
ACCESSION AF182188
VERSION AF182188.1 GI:10952509
KEYWORDS
SOURCE
ORGANISM Lotus corniculatus var. japonicus (Lotus japonicus)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.
REFERENCE 1 (bases 1 to 1797)

AUTHORS Simon, U. and Udvardi, M.K.
 TITLE cDNA encoding a putative ammonium transporter from *Lotus japonicus*
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 1797)
 AUTHORS Simon, U. and Udvardi, M.K.
 TITLE Direct Submission
 JOURNAL Submitted (01-SEP-1999) Udvardi, Max-Planck-Institute for Molecular Plant Physiology, Am Muehlenberg 1, Golm D-14476, Germany
 FEATURES
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 1..1797
 /organism="Lotus corniculatus var. japonicus"
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 /variety="japonicus"
 /db_xref="taxon:34305"
 /tissue_type="nitrogen-fixing nodules"
 76..1581
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 /protein_id="RAG24944.1"
 /translation="MALPECSAANLAOLIGNATDAVAAGFICDOFTAVGOREPSTAF
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 YLISFSLTGFVYVSWFSGGWSAINTNGLFTGVIDFAGSGVHMVWGVSAG
 LWGALIEPRIGREDHAGRAVSLRGHSASLVLTGFMWFTGFGNPGSLFKLSAYD
 SGNYYGWSAIGRTAVTTLTLAGCTAALTTLFGKRIISCHWNVTDCNGLIGFPAALTA
 GCSVVEWAAIVCGFPAVAVLIACNMLAEKRVDDPLEAOLHGGCGAWGIIITLALFA
 KEEVYVQYQPKRPRVFLFNGGKLLGHAHVILVIGWSATMGPIFLILNKWL
 LRISTEDELAGMDLTHRGSPAYAVEDDESHKPIQLKIEPNSSTPSAES"

CDS

Query Match 53.4%; Score 910.8; DB 8; Length 1797;
 Best Local Similarity 74.2%; Pred. No. 1.8e-151;
 Matches 1181; Conservative 0; Mismatches 402; Indels 9; Gaps 2;
 20 CCACCGTAGTTTCACACCTTCAGTCACGCGGTATATACATAACCAACCCACCATGTC 79
 21 CGCCTCTTGACTCTTGACTCTCCCTCTCTTCCAAAGTCACATACCCCAACAGATGCG 80
 80 GCTGCTGCTTGTCCGCGCAACAACTGGGCCAACTTCTCGGCCCAACACCAAGTCGCA 139
 81 GCTGCGGAGTGCTCGGCGGCACTAGCGAGCTCATCGGCCCAACCGCAGACAGCG 140
 140 CTCGCGCGCGCTCCCTTATCTCGGCCATTTTCGCGCGCTGAGCAGCAAGTTCTGCA 199
 141 CGCCGAGTCGCGGATTCATCTCGGACCACTTACCGCGCTGGGTCAACGATCTCCGA 200
 200 CACGCGCTTCGCGGTGACACACCTACCTCTCTTTTCGCGCTACCTGTTTTTCTAT 259
 201 CACAGCATTCGCGGTGACACACCTACCTCTCTCTTCGCGCTACCTGATTTCTGAT 260
 260 GCAGCTCGGCTTCGCCATGCTCTCGCGCGCTCGTTCGCGCGCAAGAACATGACAT 319
 261 GCAGCTCGGCTTCGCCATGCTCTCGCGCGCTCGTTCGCGCGCAAGAACATGACAT 320
 320 CATGCTCACCAACGCTTCGAGCGCTCGCGCGCGCTCTCTTACTACTCTTCGCGCTT 379
 321 CATGCTCACCAACGCTTCGAGCGCGCGCGCGCGCTCTCTTACTATCTCTCGGTTT 380
 380 CGCCTTCGCTTCGCGCTTCGCGCTTCGAGCGCTTCGAGCGCTTCGAGCGCTTCGAG 439
 381 CGCCTTCGCTTCGCGCTTCGAGCGCTTCGAGCGCTTCGAGCGCTTCGAGCGCTTCG 440
 440 GGACATCCCTTCATCTCTACGACTACGACTCTCTCTCTACCAATGGCGCTTCGCCAT 499
 441 AGAGCTCCCCACCTAGGCTTCGAGCTACGACTCTCTCTCTACGAGTGGCGCTTCGCCAT 500
 500 CGCGCGCGCGGATTCACGAGCGAGCAATCGCGCGAGCGAGCGAGCTTCGCGCTTCT 559
 501 CGCGCGCGCGGATTCACGAGCGGCTCAATCGCTGAACGACAGCTTCGCTGCTTACCT 560
 560 CATCTACTCTCTCTCTCTACCGGCTTCGCTATCGGTGCTCTCCACTGCTTCTGTC 619

ORIGIN

1040 CTGCAACGGGCTGTAGCGGGTTTCGCGCGGATAACAGCGGGTTGCTCGGTGGTGGAGCC 1099
 1038 ATGCAACGGCTTACTCGCGGGTTTCGCGCAATCACCGCGGTGCTCGGTGGAGCC 1097
 1100 ATGGGAGCCATCGTATCGGTTTCTGCTCTATAGTATTAAAGTTCGAAACAAT 1159
 1098 CTGGGAGCCATCGTATCGGTTTCTGCGCGGTTCGCGCGAGTGGTGTATCGCGGTGCAACATGCT 1157
 1160 AGCAGAGAAGGTTAAGTTTCACGATCCTCTGAGGCGCGCGAGTTGCAAGTGGGTGGG 1219
 1158 CGCAGAAAGGTGCGTTAGCAGACCCCTTAGAGGAGCTCAGCTTCACGGCGGTGGG 1217
 1220 CAGTGGGGGTGATATTCACGCGTTGTCGCAAAAGGAGTATGTGAAGAGGTTTA 1279
 1218 CGGTGGGGGATCATATTCACCGCGTATTCGCGAGGAGGAGTACGTGAACAGGTTTA 1277
 1280 CGGGTT-----GGGAGGCGCGCAGCGGTGCTCATGGGGGTGGTGGAGTTCGTCG 1333
 1278 CCGGGTAAACCGGGTCGCCATACGGGTTGTTTCATGGGTGGTGGAGGAGCTGCTCGG 1337
 1334 GGCGCAGTGATTCAGATTCGTGATTCGCTGGGTGGGTAGTTCGAGCCATGGGACCTT 1393
 1338 AGCGCAGTGATCCAGATTTTGGTGAATATCGGTTGGGTTCAGCGCCACAATGGGTCTCT 1397
 1394 GTTTTGGGGTTCGAAATAAAGTGAAGCTGTGAGGATTTCTTCAGAGGATGAGCTTCGCGG 1453
 1398 GTTCTTCTTCTGAATAAGATGAATGATGCTTCGAGTCTCAAGGAGGATGACTTCGCGG 1457
 1454 GATGAGCATGATCTCGCCATGGAGGCTTTCGCTTATGCTTATGAGGATGATGAGACGCA 1513
 1458 TATGAGTCTGACCCGACATGCTGGGTTTGCATATGATGAGGATGATGAATCGACAA 1517
 1514 GCATGGATGAGTTCGAGGAGGTTGGGCGCAACCGCTTCTCCACACCCACCATGATGA 1573
 1518 GCCAGGATTCAGTACGGAAGATTGAACCTTAACCTTCTTCCACTCTCTAGTGTGATGC 1577
 1574 ATGATCTTTTTTCCCATATGATGCTCAAT 1605
 1578 ATGATAATAATAGTAGTAATAATTTTCGTTTT 1609

RESULT 2
 AY135020

LOCUS
 DEFINITION Lotus japonicus ammonium transporter (Amt1,2); mRNA, complete cds.
 ACCESSION AY135020
 VERSION AY135020.1 GI:31322043
 KEYWORDS
 SOURCE
 ORGANISM
 Lotus corniculatus var. japonicus (Lotus japonicus)
 Lotus corniculatus var. japonicus
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
 Lotus.
 1 (bases 1 to 1557)
 El Alaoui, H. and Chiurazzi, M.
 Characterization of a new ammonium transporter in Lotus japonicus
 Unpublished
 REFERENCE
 2 (bases 1 to 1557)
 El Alaoui, H. and Chiurazzi, M.
 Direct Submission
 Submitted (23-JUL-2002) Plant Biology, Institute of Genetics and
 Biophysics 'Adriano Buzzati Traverso', Via Marconi, 12, Naples
 80125, Italy
 FEATURES
 Location/Qualifiers
 1..1557
 /organism="Lotus corniculatus var. japonicus"
 /mol_type="mRNA"
 /variety="japonicus"
 /db_xref="taxon:34305"
 /ecotype="GIFU"
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 /gene="Amt1,2"
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 /gene="Amt1,2"
 /note="putative Amt1,2"
 /codon_start=1
 /product="ammonium transporter"
 /protein_id="IAM95453.1"
 /db_xref="GI:31322043"
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 PAFAPGASNGFIGNHFGLHSPYDYSFLLQWAFIAAAGITSGSIAERTQV
 AYLIVSFLTFGVVPSVHWSMDGWSAPTRTTGSLFGSGLDIDFAGSVVHMGVI
 AGLWAFLEGRIPTGRTSVLRGHSASLVVGLFWFGVFNFGSFLTIKA
 YGNGENNYVQWSAIGRTAVTTLAGCTAAATLTPSKRLHGHKWLVDVNGILGG
 FAATSGSVYVPPWPAIVCGFVAWVLIQLNVAAMKVDPLDLEAQLHGGCGMGL
 FTGLPAKGEVVAEVVGSAGREYGLMGSGKLLAAQVIELVVGWVTAIMPFLFGL
 HKTKLLRISEDETAGMDLFRHGFPAYAHDDDDVSTRGVMSRIGPGSGSPSTWNT
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 ORIGIN
 Query Match 48.8%; Score 832.8; DB 8; Length 1557;
 Best Local Similarity 74.0%; Pred. No. 1.2e-137;
 Matches 1117; Conservative 0; Mismatches 372; Indels 21; Gaps 4;
 QY 78 TCGCTGCTGCTTGTCCCGCGGACAACTGGCCCAATCTTCGCGCCCAACACACAGAC 137
 Db 7 TCTCTCTCTTGTCTGAGCAGACAGCTCGCTCCACTCTTAACCGCCCAACACCAACGCAAC 66
 QY 138 GCCTCCGCGCGCGCTCCCTTATCTGCGGCCATTTTCGCCCGCTGGACAGCAAGTTCGTC 197
 Db 67 GCAACCGCGCGCGCACTACTCTGCAACGAGCTCGATCAATCTCCAGGAAGCTCAGC 126
 QY 198 GACAGCGCTTCGCGGTGCAACCACTACTCTCTTTTCGCCCTACCTCGTTTTCCT 257
 Db 127 GACACCACTTATGCGGTGCAACCACTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 186
 QY 258 ATGCAGCTCGGCTTCGCGCATCTCTGCGCGGCTCGCTCGCGCCGCAAGACCACTGAC 317
 Db 187 ATGCAGCTCGGCTTCGCGCATCTCTGCGCGGCTCGCTCGCGCCGCAAGACCACTGAC 246
 QY 318 ATCATGCTACCAACGCTCTGAGCGCTGCGCGCGGCGGCTCTTCTTACTACCTCTTCGGC 377
 Db 247 ATCATGCTACCAATGTTCTTGTATGACGAGCGCGCGGCGGCTCTCTTACTACTCTTCGGC 306

378 TTGCGCTTCGCTTTCGGTTCCTCCCTCCACGCGTTCATCGGTAAACATTTCTTCGGCTC 437
 Db TTGCGCTTCGCTTTCGGAGCGCCCTCCAAACGGCTTCATCGCGCCACTTCTTCGGCTC 366
 QY 438 AAGGACATCCCTTCATCTCTCTAGCTACAGCTACTTCTCTACCAATGGGCTTCGCC 497
 Db AAACACTTACCTTTCGCCCACTTACGCTACAGCTTCTTCTCTACCAAGTGGGCTTCGCC 426
 QY 498 ATGCGCGCGCGCGCATCACACAGCGGAAGCATCCGCCAAAGCACACAGTTCGTTGCCCTAT 557
 Db ATGCGCGCTGCGGGAATCACACAGCGGTCCATCGCGGAGGACACAAATTCGTCGCTAC 486
 QY 558 CTCATCTACT 617
 Db CTCATCTACT 546
 QY 618 TCCCGAGACGGCTGGGCTCTGCGCTTTAAAGATACCCGACCG---GCTATTTTCACCGGC 674
 Db TCTCGGACGGCTGGGCGAGCCCAACCGGACCACTGGCAGCTTACTATTTCGATCCGGC 606
 QY 675 GTAATAGACTTCGCGGTTCCGGGTAGTGCATATGTCGCGGAATAGCGGCTATGG 734
 Db GCGATTGATTTCGCTGGATCCGAGTAGTCCACATGGTTCGCTGGCATAGCAGACTATGG 666
 QY 735 GGAGCGCTGATCGAAGGCCCAAGAAATGGGACGTTTCGATCATGCGGACGAGCTGTGGCC 794
 Db GCGCGCTTCATCGAAGGCCCTAGAAATCGCGCGTTTCGACCGAACCGGCGATCCGTAGCC 726
 QY 795 TTGAGGCGCACAGCGGCTCTTAGTAGTCTCTGAGAACCTTCTTGTGTTTGGTTTCGTTGG 854
 Db TTAGCTGACACAGTGCCTCTCTAGTTTGTCTCGGTTCTCTTACTATGTTTCGTTGG 786
 QY 855 TACGGAATTAACCCCGGTTCAATTTAAACAAATCTCTTACTTACGTAACCTCAGAA--- 911
 Db TACGGTTTCAACCCCGGTTCAATTTCTCACCATAGCAAAAGCTTACCGTACACAGCGGAA 846
 QY 912 -----AATTACTACGTTCAATGAGCGCGGTTGGCAGAACCGGCTCACCACTACCTA 965
 Db AACGGTAATTAACGTTCAAGTGGAGCGCATAGGAGAAACAGCGGTCAACACCACTG 906
 QY 966 CGCGGGTCAACAGCTGCTTGACACAGCTATTCCGTAACAGGGTGATACCGGTCACTGG 1025
 Db GCTGATGCACTGCGGCACTCAACACGCTTTTTCAGCAACGTTTATGGAGGCGCACTGG 966
 QY 1026 AACGTACCGATGTCGCAACGCGGCTTTAGCGGTTTCGCGCGGATAACAGCGGTTGC 1085
 Db AAGTGTCTGACGTGTGTAACGCGCTGCTCGCGGTTTCGCGCCATCACTCCGTTGC 1026
 QY 1086 TCCGTGTTGAGCCATGGCGAGCATCGTATCGGTTTGTGTTGCTTCTATAGTATTAATA 1145
 Db TCCGTGTTGAGCCGTTGGCGCGGATGTTGTTGCGGTTTGTGCGAGCGTGGGTGCTGATC 1086
 QY 1146 GCTTGCACAAATTAGCAGAGAAAGTTAAGTTTCGACGATCCTCTGAGGCGCGCGCATG 1205
 Db GGGTCAATTTGGTTGGCGGCAAAATGAAGTACGACGATCCTCTGGAGCGCGCGAGCTT 1146
 QY 1206 CAGGTGGGTGTCGACGCTGGGGGTGATTTACCGCGTTGTTTCGAAAAAGAGATAT 1265
 Db CAGCGGGGTGCGCGCGCTGGGGGTTTATTACCGGGCTGTTTCGAAAGGGGAGTAC 1206
 QY 1266 GTGAAGAGAGTTTACG---GGTTGGGGAGGGGCGACGCGTGTCTCATGGGGGTGGTGGG 1322
 Db GTGGCGAGGTTTACGCGAGCGCTGGGAGCGCGTACGGGTTGTTAATGGTGGCGGAGG 1266
 QY 1323 AGTTGCTGGCGGCGACGCTGATTAGATTTCTGGTGAATTCGTTGGGTGGGTAGTGGGAC 1382
 Db AGTTGCTGGCGGCGAGGTTAGATTTTGGTGGTGTGTTGGGTGGGTTACCGCGAGC 1326
 QY 1383 ATGGGACCTTGTGTTTGGGGGTTGAATAAAGCTGTTGAGGATTTCTTCAGAGAT 1442
 Db ATGGGCGGTTGTTCTATGGGCTTCATAGACGAACCTTTGAGGATTTCTGAAGATGAT 1386
 QY 1443 GAGCTTGGGGGATGACATGATCTGCCATGAGGCGTTTGTATGCTT-----ATGAG 1496

Db 1387 GAGACTGGGGGATGATTTGACGAGGATGTTGGTTGCTTACCATGATGAT 1446
QY 1497 GATGATGAGACCAACAGATGGGATGAGTTGAGGAGGTTGGCCCAACGGCTTCTCC 1556
Db 1447 GATGATGTTGTCACCAAGAGAGGGGTCATGATGATGATGATGATGATGATGATGAT 1506
QY 1557 ACACCCACCA 1566
Db 1507 CCTCCACCA 1516

RESULT 3
BT009318
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BT009318 1991 bp mRNA linear PLN 20-JUN-2003
Triticum aestivum clone wlm12.pk0020.b10.fis, full insert mRNA
sequence.
BT009318
BT009318.1 GI:32128869
FLI CDNA.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poaceae; Triticeae; Triticum.
1. (bases 1 to 1991)
Tingley,S.V., Wolters,P., Powell,W., Dolan,M., Miao,G.-H.,
Caraher,N.R., Hanafey,M.K. and Hainey,C.F.
Direct Submission
Submitted (20-JUN-2003) Crop Genetics, E. I. DuPont de Nemours and
Company, 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104,
USA

FEATURES
source
Location/Qualifiers
1..1991
/organism="Triticum aestivum"
/mol_type="mRNA"
/db_xref="taxon:4565"
/clone="wlm12.pk0020.b10.fis"

ORIGIN

Query Match 45.1%; Score 768.6; DB 8; Length 1991;
Best Local Similarity 73.8%; Pred. No. 2.9e-126;
Matches 991; Conservative 0; Mismatches 349; Indels 3; Gaps 1;

QY 174 GCGCGCGTGGACAGCAAGTTCGTGACACGGCCTTCGCCGTCGACACACCTACCTCTC 233
Db 134 GACTACCTGTGACACAGTTCCGCGACACACAGTCCCGGTGACCTACCTACCTGCTC 193
QY 234 TTTTCGGCTACCTCGTTTTTCTATGACGCTCGGCTTCGCCATGCTCTGCGCGGCTCC 293
Db 194 TTCTCGGCTACCTCGTTCGCCATGACGCTCGGCTTCGCCATGCTCTGCGCGGCTCC 253
QY 294 GTCGCGCCAGACACCATGACATGCTGACCAACGTCCTGGAAGCTGCGCGGCGG 353
Db 254 GTCCGGGCAAGACACCATGACATGCTGACCAACGTCCTGGAAGCTGCGCGGCGG 313
QY 354 GGCCTCTTTACTACTCTTCGGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGAAGGCTTC 413
Db 314 GCGCTCTTTACTACTCTTCGGGCTTCGGCTTCGGCTTCGGGACGCGGTGGAAGGCTTC 373
QY 414 ATCGGTAAACATTTCTCGGCTCAAGGACATCCCTTCATCTCTTCAGCTACAGCTAC 473
Db 374 ATCGGGAAGCACTTTCTGGGCTCAAGGACATGCCGACAGCGGCTTCGACTACAGCTTC 433
QY 474 TTCTCTACCAATGGGCTTCGCCATCGCGCGCGCGGACATCAAGCGGAAGCATCGCC 533
Db 434 TTCTCTTTCCAGTGGGCTTCGCCATCGCGCGCGCGGACATCACTTCGGCTCCATCGCC 493
QY 534 GAAACGACAGTTCGGGCTATCTCATCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCT 593
Db 494 GAGAGGACGAGTTCGGTGGGCTATCTCATCTACTCTCGGCTTCCTTACGGGANTCGCTAC 553
QY 594 CCGGTGGTCTCCCACTGGTCTGTGTCGCCAGACGGCTGGGCTCTGCTTTAAGATCACC 653

Db 554 CCGTCTGTGTCACCTGATCTGGTCCGTGACGGGTGGGCTTCGCGCGCCCGCAGCTCC 613
QY 654 GACCGGCTATTTTTCAC 710
Db 614 GCGCGGCTGTCTTCAAGTCCGGGCTGATGACATCTTCGCGGCTTCGCGGCTGTCGACATG 673
QY 711 GTCGCGGAATAGCCGCTATGCGGAGCGCTGATCGAAGGCGCCAGAAATGGGAGCTTTC 770
Db 674 GTCGCGGATCGCGGCTTCTGGGCGGCTCATCGAGGCGCCCGCATCGCGCGGCTTC 733
QY 771 GATCATGACGACGAGCTGTGGCTTTCGAGGCGCACAGCGCGCTCTTAGTCTCTGGGA 830
Db 734 GACACGCGCGGCTCGGTGGGCTCAAGGCGCACAGCGGCTGCTCGTCTGCTGGG 793
QY 831 ACCTTCTGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 890
Db 794 ACCTTCTGCTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 853
QY 891 CTTACTTACGTTAACTCAGGAATTTACTACGGTCAATGAGCGCGGTTGGCAGAACCGCG 950
Db 854 AAGTGTGACGCGCGCGCGGAGCATCAAGGCGAGTGTTCGGGCTGGCGCGCACCGCC 913
QY 951 GTACCACTACCTAGCGGCTCAACAGCTGCTTGAACACCTATTCGGTTAAACGGGTG 1010
Db 914 GTGACGACGACGCTGCGGCGGCGGCTCAGCAGCTGTTCGGGAAGCGGCTC 973
QY 1011 ATATCCGCTCACTGGAACGTGACCGATGTCGACGCGCTGTAGGCGGTTTCGCGCGG 1070
Db 974 CAGACGGGCACTGGAACGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1033
QY 1071 ATACAGCGGTTGCTTCGGTGTGAGCCATGGGACGCTATGCGGTTTGTGTTGTTGTTGTT 1130
Db 1034 ATACCGCGGCTGACGCTGTTGCGACCGCTGGCGCGCTCATCTCGGCTTCGCTCC 1093
QY 1131 TCTATGATTTATAGCTTGCAACAAATTAGCAGAGAGTTAAGTTGACGATCCTCTG 1190
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KEYWORDS
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ORGANISM

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Sequence 423 from Patent WO0222675.
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Arabidopsis thaliana

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REFERENCE

AUTHORS

TITLE

JOURNAL

JOURNAL

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Glazebrook, J., Wang, X., Dangl, J.L., Eulgem, T. and Zhu, T.

Plant genes, the expression of which are altered by pathogen infection

Patent: WO 0222675-A 423 21-MAR-2002;

Syngenta Participations AG (CH); UNIVERSITY OF NORTH CAROLINA AT

CHAPL HILL (US); Glazebrook, Jan (US); Wang, Xun (US); Dangl,

Jeffrey L. (US); Eulgem, Thomas (US)

Location/Qualifiers

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Matches 1036; Conservative 0; Mismatches 397; Indels 12; Gaps 3;

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Query Match 44.3%; Score 755.8; DB 6; Length 1506;
Best Local Similarity 71.7%; Pred. No. 5.4e-124;
Matches 1036; Conservative 0; Mismatches 397; Indels 12; Gaps 3;

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SOURCE Arabidopsis thaliana (thale cress)
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REFERENCE
1 Ninnemann, O., Jauniaux, J.C. and Frommer, W.B.
Identification of a high affinity NH4+ transporter from plants
EMBO J. 13 (15), 3464-3471 (1994)
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PUBMED 8062823
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Direct Submision
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ORIGIN

Query Match 44.3%; Score 755.8; DB 8; Length 1700;
 Best Local Similarity 71.7%; Pred No. 5.4e-124;
 Matches 1036; Conservative 0; Mismatches 397; Indels 12; Gaps 3;

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DB	544	GGTCAATGATGATGGCGCGCGCTTCGCTACCGATGAGATTTGCTTTTCAGCACCG	603
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QY	853	GGTAGGATTTAAACCGGCTTCAATTAACAACTCTTACTTACGTAGTAACTAGGAA	912
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 ACCESSION A44314
 VERSION A44314.1 GI:2299142
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 ORGANISM Arabidopsis thaliana
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 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
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 DNA SEQUENCES FOR AMMONIUM TRANSPORTER, PLASMIDS, BACTERIA, YEASTS,
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 PATENT: WO 9511978-A 1 04-MAY-1995,
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Best Local Similarity 71.7%; Pred. No. 5.4e-124;
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256  CTATGCAGCTCGGCTTCGCCATGCTCTGCGCGGCTCCGTCGCGCAAGACACATGA 315
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316  ACATCATGCTCACCAAGCTCTGACAGCTCCGCGCGGCTCTTCTACTACCTCTTCG 375
    Db          ACATCATGCTTACCAACGCTCTGACGCTGCAGCGGTGCTCTTCTTATATCTGTTG 303
376  GCTTCGCGCTTCGCTTCGGCTCCCGCTCCGACGGCTTCATCGTAAACATTTCTCGGC 435
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Qy          1447  TTGCGGGATGACATGCTCCGATGAGGCTTTCGCTTATGCTTATGAGGATGATGAGA 1506
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DEFINITION Sequence 1 from patent US 6620610.
ACCESSION AR399484
VERSION   AR399484.1 GI:40141532
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SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 1748)
AUTHORS  Frommer,W.-B. and Ninnemann,O.
TITLE     DNA sequence from Arabidopsis thaliana encoding ammonium
transporter, and plasmids, bacteria and yeast comprising the DNA
sequence
JOURNAL   Patent: US 6620610-A 1 16-SEP-2003;
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Best Local Similarity 71.7%; Pred. No. 5.4e-124;
Matches 1036; Conservative 0; Mismatches 397; Indels 12; Gaps 3;
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Qy	616	GGTCCCGACAGCGCTGGGCTCTGCTCTTAAAGATCACCGACCGGCTATTTTCCACG	672
Db	544	GGTCAGTTGATGAGTGGCGAGCGGCTCGTACCGATGGAAATTTGCTTTTCAGACCG	603
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ACCESSION	AL049656		
VERSION	AL049656.1	GI:4678371	
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SOURCE	Arabidopsis thaliana		
ORGANISM	Arabidopsis thaliana		
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AUTHORS	2	(bases 1 to 113970)	
JOURNAL	EU Arabidopsis sequencing, project.		
REFERENCE	2	(bases 1 to 113970)	
AUTHORS	Submitted (19-APR-1999)	MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitze 18a, D-82152 Martinsried, FRG, E-mail: schueller@mps.biochem.mpg.de, mayer@mps.biochem.mpg.de	
TITLE	Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK, E-mail: michael.bevan@bbsrc.ac.uk		
JOURNAL	Information on performance of analysis and a more detailed annotation of this entry and other sequences of chromosomes 3, 4 and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/ .		
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27751-27983 and 28079-28154; no obvious
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obvious
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/translation="MAAKFRISSSSFHSHRASDSSTSSSSSYSGLLALPQFCPPSPLG
PPEFLKHLKGGGDEVKPKDKKXKITKEBEPEQYQWQVGERGEMPMKTPFLPIIF
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		/gene="T6G15.50"	/number=1	/number=2	/number=3	/number=4	/number=5	/number=6	/number=7	/number=8	/number=9	/number=10	/number=11	/number=12	/number=13	/number=14	/number=15	/number=16	/number=17	/number=18	/number=19	/number=20	/number=21	/number=22	/number=23	/number=24	/number=25	/number=26	/number=27	/number=28	/number=29	/number=30	/number=31	/number=32	/number=33	/number=34	/number=35	/number=36	/number=37	/number=38	/number=39	/number=40	/number=41	/number=42	/number=43	/number=44	/number=45	/number=46	/number=47	/number=48	/number=49	/number=50	/number=51	/number=52	/number=53	/number=54	/number=55	/number=56	/number=57	/number=58	/number=59	/number=60	/number=61	/number=62	/number=63	/number=64	/number=65	/number=66	/number=67	/number=68	/number=69	/number=70	/number=71	/number=72	/number=73	/number=74	/number=75	/number=76	/number=77	/number=78	/number=79	/number=80	/number=81	/number=82	/number=83	/number=84	/number=85	/number=86	/number=87	/number=88	/number=89	/number=90	/number=91	/number=92	/number=93	/number=94	/number=95	/number=96	/number=97	/number=98	/number=99	/number=100	/number=101	/number=102	/number=103	/number=104	/number=105	/number=106	/number=107	/number=108	/number=109	/number=110	/number=111	/number=112	/number=113	/number=114	/number=115	/number=116	/number=117	/number=118	/number=119	/number=120	/number=121	/number=122	/number=123	/number=124	/number=125	/number=126	/number=127	/number=128	/number=129	/number=130	/number=131	/number=132	/number=133	/number=134	/number=135	/number=136	/number=137	/number=138	/number=139	/number=140	/number=141	/number=142	/number=143	/number=144	/number=145	/number=146	/number=147	/number=148	/number=149	/number=150	/number=151	/number=152	/number=153	/number=154	/number=155	/number=156	/number=157	/number=158	/number=159	/number=160	/number=161	/number=162	/number=163	/number=164	/number=165	/number=166	/number=167	/number=168	/number=169	/number=170	/number=171	/number=172	/number=173	/number=174	/number=175	/number=176	/number=177	/number=178	/number=179	/number=180	/number=181	/number=182	/number=183	/number=184	/number=185	/number=186	/number=187	/number=188	/number=189	/number=190	/number=191	/number=192	/number=193	/number=194	/number=195	/number=196	/number=197	/number=198	/number=199	/number=200	/number=201	/number=202	/number=203	/number=204	/number=205	/number=206	/number=207	/number=208	/number=209	/number=210	/number=211	/number=212	/number=213	/number=214	/number=215	/number=216	/number=217	/number=218	/number=219	/number=220	/number=221	/number=222	/number=223	/number=224	/number=225	/number=226	/number=227	/number=228	/number=229	/number=230	/number=231	/number=232	/number=233	/number=234	/number=235	/number=236	/number=237	/number=238	/number=239	/number=240	/number=241	/number=242	/number=243	/number=244	/number=245	/number=246	/number=247	/number=248	/number=249	/number=250	/number=251	/number=252	/number=253	/number=254	/number=255	/number=256	/number=257	/number=258	/number=259	/number=260	
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QY	1273	AGGTTTACGGTTG-----GGAGGGCGCACGGGTTCCTCATGGGGGTGGTGGGAAGT	1326
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Db	44234	CTAAT 44238	
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LOCUS	ATCHRIV36	199634 bp	DNA linear
DEFINITION	Arabidopsis thaliana DNA chromosome 4, contig fragment No. 36.		
ACCESSION	AL161536		
VERSION	AL161536.2	GI:7268028	
KEYWORDS			
SOURCE	Arabidopsis thaliana (thale cress)		
ORGANISM	Arabidopsis thaliana		
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi		
REFERENCE	1 (bases 1 to 47586; 47571 to 111411)		
AUTHORS	Pohl, T., Weizenecker, T., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.		
REFERENCE	Unpublished		
AUTHORS	2 (bases 46394 to 47589)		
	Robben, J., Grymonprez, B., Volckaert, G., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.		
JOURNAL	Unpublished		
REFERENCE	3 (bases 102208 to 102209)		
AUTHORS	Murphy, G., Ridley, P., Hudson, S., Mewes, H.W., Lemcke, K. and Mayer, K.F.X.		
JOURNAL	Unpublished		
REFERENCE	4 (bases 1 to 199634)		
AUTHORS	EU Arabidopsis sequencing project.		
TITLE	Direct Submission		
JOURNAL	Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer Biochemie, Am Klopferspitze 18a, D-82152 Martinsried, FRG, E-mail:		

lemcke@mps.biochem.mpg.de, mayer@mps.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbc.ac.uk
Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>
this fragment has an overlap with ATCHRIV35 at the 5' end and an
overlap with ATCHRIV37 at the 3' end.

COMMENT

FEATURES

Location/Qualifiers
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/mol_type="genomic DNA"
/variety="Columbia"
/db_xref="taxon:3702"
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repeat_region

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/gene="AT4g13260"

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9680..10357))

/gene="AT4g13260"

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9680..10357))

/gene="AT4g13260"

/notes="similarity to dimethylalanine monooxygenase

(N-oxide-forming) (EC1.14.13.8) -Oryctolagus cuniculus,

PID:gi64989

Contains Prokaryotic membrane lipoprotein lipid attachment

site AA33-43"

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NAEVPEDIDIPFGPILHTSSYSKSGIFSEKKILVVGCGNMGVECLDCNPNAL

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/number=3

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/note="codon recognized: CUU"

18021..18599

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18021..18599

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thaliana"

/codon_start=1

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/db_xref="GOA:Q9T0J9"

/db_xref="SPTRMBL:Q9T0J9"

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ILKPVWMLSSQDDTSKRVLLQLLSLGLAFHENEIKNLSHARKIDDTG
DEKDLSTISIMPRVFTYGNLPSVFRFTGDDGKFOQLSTEDAKGILSYEAHLG
TTDYLDLAKFTSSHLKSLAGTCRPHLRILNTLYLPQRWNEAVIARYISF
YEQEDHDMLRLAKNFKLLQLHYIKELSKFIKNWMLGLTSKWPSPRIVEAW
LAGLMVPEPQPSGGRVIAKFNLYLTLDACDHYFISHELTRLVACVWRWSPDGID
TLEDISRSVFKMLDVPDDIGKVSRSBSSVHLKEMLEELNLRANLDLVKWARGIQ
VPSFEHVEVGIIASVATLWVSFGMGETAGKEAVENVFLVCSQPMSPGFAANLN
VYMKQFVTKREALECCRMIVDINKTINBELLTSTVPRVRLKQALNFRLLLELIT
KSDIYNSGKRLKRIIVTLLIDFRL"
complement(19902..20216)
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/number=1
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/gene="AT4g13280"
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exon

intron

exon

intron

exon

intron

exon

intron

exon

intron

exon

intron

exon	complement (23385..23486)	QY	733	GGGAGGCGCTGATCGAAGCCCAAGAAATGGGACGCTTTCGATCATCGAGGAGCGAGTGGG	792
gene	/gene="A74g13280"	Db	145605	GGGCTGGCTCATCGAAGGTCACGACTTGGCGGTTGATAACGAGCGCGTGCCATCG	145664
CDS	27422..29411	QY	793	CTTGGAGGCGCACAGCGGTCCTTAGTAGTCTCTGGGAACCTTCTTGTCTTGGTTCGGTT	852
	/gene="A74g13280"	Db	145665	CTCTCTGTGGCCACTCGGCGTCACTTGTGTCTTGGGAACATCTCTCTGTGTGGAT	145724
	/notes="strong similarity to cytochrome P-450LXXIAl, Persea	QY	853	GGTACGGAATTAACCCCGGTTCACTTTAAACAAATCTTACTTTACCGGTAACTCAGGAA	912
	americana, M32885	Db	145725	GGTACGGAATTAACCCCGGTTCTTCAACAGATCTTAGTCACTACGTAACGAGA--CAGGCA	145781
	contains Cytochrome P450 cysteine heme-iron ligand	QY	913	ATTTACTACGCTCAATGAGCGGCTTGGCAGAACCGCGTCACTACCTACCTACCGGGGT	972
	signature AA426-435	Db	145782	CATACACCGCGGCTGAGCGCGTTCGAGCAGACAGCTGTACACAAACAGTTAGTCTGCT	145841
	contains EST gb:A1999004.1"	QY	973	CAACAGCTGCTTTGACCACGCTATTTCGTTAAACGGGTGATATCCGGTCACTGGAACGTGA	1032
	/codon_start=1	Db	145842	GCACCGCGGCTGACAAACCTATTTTGGGAAACGCTACTCTCGGGAATTTGGAACGTCA	145901
	/product="cytochrome p450-like protein"	QY	1033	CCGATGCTCGAAGCGGCTGTTAGCGGCTTTCGCGCGATACACGCGGTTGCTCCGCTG	1092
	/protein_id="CAB78371.1"	Db	145902	CTGATGATGCAACCGGCTCTCTCGAGGGTTTTCAGCCATTAACCTGCTGCTCTGCTG	145961
	/db_xref="GI:7268032"	QY	1093	TTGAGCCATCGGCGACCATCGTATCGGTTTTTGTGCTTCTATAGTATTAATAGCTTGA	1152
	/db_xref="GOA:Q9TOK0"	Db	145962	TTGAGCCATCGGCTGCGATCATCTCGGCTTCTGTCGGCGCTAGTCTCTCTCTGATGCA	146021
	/translation="WEILVTLTLLTLLALLLLKSLKRTTNNLNPSPWRLPVIG	QY	1153	ACAAATTAGCAGAGAGGTTTAAAGTTCGACGATCTCTGGAGCGCGCGAGTTGACCGGTG	1212
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	TKVIDKILGRSDVAPAPGYEYKMKKSICIONLLSNKMSYKIKPEDRIKLMIEKV	QY	1213	GGTGTGACAGTGGGGGTGATATTACCGGCTTTCGCAAAAAGGAGTATGTGAAGG	1272
	EHASSCSPPSNLSQFLWLTNDLICRAALGRKYSSKEDGIDVENIVRAFSALVEF	Db	146082	GTTCGGGTGCGTGGGACTAATATTACCGCTCTCTCTGCTCAAGAAAGTACTTTGAACC	146141
	PGEYIPLSUSWDIKIRGQKHQVEEDVKRPFLEVRVKEHEDANKDRTSRDVLTLTI	QY	1273	AGTTTACGCGTTG-----GGAGGCGCACGCGTCTCATGGGGGTGCTGGGAAGT	1326
	QDSKALKLIIDMFLAGTATSLSLFWAMTLMRNPKVMKQOEIRSSRSQGLFTV	Db	146142	AGATTTACGCAACAAACCCGAGGACACAGGTTTGTATTAGCGGTGAGGAAAC	146201
	EKEAEMDYLQAVIEKALRPAPLMVRFVSEDTLKGYNIPAGTQVLIINAWIQR	QY	1327	TGCTGGCGGCGCATGATTCAGATCTTGGTGAATTCCTGGGTGGGTAGTGGCCCATAG	1386
	DTTWGIDAEFRPRLHLSILDFOQDFKFIPIFGSKRICPGIGFTSALIGVTLNI	Db	146202	TACTTGGAGCTCAGCTGATTCAGATCAATTTGATCACGCGTTGGGTAAAGTGGCCATAG	146261
	VKRFNRMDVEPQVQHDLTATGLVWFKPLIAPSSA"	QY	1387	GACCTTGTCTTGGGGTGAATAAAGTCTGTAAGCTCTGAGGATTTCTTCAGAGGATGAGC	1446
	27422..27808	Db	146262	GGACACTTTCTTCATCTCCCAAGAAATGAAATGTTGCGGATATCTGTCGAGATGAGA	146321
	44.3%; Score 755.8; DB 8; Length 199634;	QY	1447	TTGCGGGAATGACATGATCGCCATGAGGCTTTGCTTATGCTTATGAGGATGATGAGA	1506
	Best Local Similarity 71.1%; Pred. No. 5.5e-124; Indels 12; Gaps 3;	Db	146322	TGGCGGATGAGATATGACGAGCGGCTGGTGTGCTTATATGATGATGATGATG	146381
	Matches 1036; Conservative 0; Mismatches 397;	QY	1507	CGCACAGCATGGGATGCGATTTGAGGAGGTTGGGCCCAACCGCTCTTCCACACCCACCA	1566
		Db	146382	AGTCTCAAGCCATTCAGCTTAGAGAGTTGAGCCACGATCTCTCTCTCTCTGCTG	146441
		QY	1567	CTGAT 1571	
		Db	146442	CTAAT 146446	

RESULT 11

AP004059/c

LOCUS

DEFINITION

Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 2,

BAC clone:OJ1372_D06, complete sequence.

ACCESSION

AP004059

VERSION

AP004059.2

GI:38093235

KEYWORDS

HTG.

SOURCE

Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Db	1032	ATCACCGCGGTTCCTCGTCTCGACCCGTGGCCGCGATCATCTCGGGTTCTCTCG	1091
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Db	1092	GGTGGGTGCTCATCGGCTCAACGCCCTGGCGCGAGGCTCAGTTTCAACGCCGCTC	1151
Qy	1191	GAGGCGGCGCAGTTTCACGTTGGTGTGGCACGTGGGGGTGATATTCACGCGCTTGTTC	1250
Db	1152	GAGGCGGCGCAGCTGTCACGCGGGTGGCGGCGTGGGGGTCACTTTCACGCGCTGTTTC	1211
Qy	1251	GCACAAAAGAGTATGTCAAGAGGTTTACGG--GTTGGGAGGGCGCACGGGTTGCTC	1307
Db	1212	GTCGCGCAGGAGTACGTGACAGATCTTCGGCCACCCGCGGCGCGTAGCGGCTGTC	1271
Qy	1308	ATGGGGGTGTGTGGAAATTGCTGGCGCGCACGTGATTCAGATTTCTGTTATGCTGGG	1367
Db	1272	ATGGCGCGCGCGCGCGCTGCTCGGGCGCACATAGTGTTCATCTGTTATCGCGCG	1331
Qy	1368	TGGGTTAGTGCACCATGGACCTTGTGTTTTGGGGGTGAAATAAACTGAAGCTTTGAGG	1427
Db	1332	TGGGTGAGCTTCAACATGGCGCGCTGTTCCTGTGCTCAACAAGCTGGGCTTCGCGC	1391
Qy	1428	ATTCTCTTCAGAGGATGAGCTTTGGGGGATGAGCATGACTCGCCATGAGGCTTTGCTTAT	1487
Db	1392	ATCTCGCGCAGGACGAGATGGCCGCGATGGACCGCGCACGGGGTTCGCTAC	1451
Qy	1488	GCTTATGAGGATGATGAGCG	1508
Db	1452	GCGTACCAACGACGACGCGG	1472

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RESULT 13
AP004053/c
LOCUS
DEFINITION
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OJ1234_B11, *** SEQUENCING IN PROGRESS ***.
ACCESSION
AP004053
KEYWORDS
HTG; HTGS_PHASE2.
SOURCE
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Oryza sativa nipponbare (GA3) genomic DNA, chromosome 2, BAC
clone:OJ1234_B11
JOURNAL
Published Only in Database (2001)
REFERENCE
2
(bases 1 to 128913)
AUTHORS
Sasaki, T., Matsumoto, T. and Yamamoto, K.
JOURNAL
Direct Submission
Submitted (15-AUG-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakienas.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT
The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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/organism="Oryza sativa (japonica cultivar-group)"
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RESULT 14

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 ACCESSION AK073718.1 GI:32983741
 VERSION AK073718.1
 KEYWORDS FLI cDNA; CAP trapper.
 SOURCE Oryza sativa (japonica cultivar-group)
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyte; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE

1
 AUTHORS The Rice Full-Length cDNA Consortium, National Institute of Agricultural Sciences Rice Full-Length cDNA Project Team:
 Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Iida, Y., Masuda, H., Ooka, H., Hotta, I., Kojima, K., Nishikawa, M., Yamada, H., Hotta, I., Kojima, K., Li, C., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group: Ohtsuki, K., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurotsaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Nakikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yamada, H., Kawai, J., Kusumegi, T., Oka, M., Ryū, R., Ueda, M., Matsubara, K., Murakami, K., Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Ota, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.
 Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

SCIENCE 301 (5631), 376-379 (2003)
 JOURNAL MEDLINE 22752273
 PUBMED 12869764

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2 (bases 1 to 2044)
 AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, Y., Iida, Y., Ikeda, R., Imamura, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M.,

Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kurotsaki, T., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murata, M., Nagata, T., Nakamura, K., Nishikawa, R., Nishikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Ohtsuki, K., Ryū, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shihata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sugabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Takagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Fahsig, W., Yanada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.
 Direct Submission
 Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agricultural Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression: 2-1-2 Mannonndai, Tsukuba, Ibaraki 305-8602, Japan (E-mail: skikuchi@nias.affrc.go.jp, Tel:81-29-838-7007, Fax:81-29-838-7007)

COMMENT This clone is one of the 28K full-length cDNA clones from japonica rice.

URL : http://cdna01.dna.affrc.go.jp/cDNA/
 NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Nishikawa, R., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohtsuki, K., Shishiki, T. and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ohtsuki, K., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurotsaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Nishikawa, R., Niikura, J., Oka, M., Ryū, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K. and Murakami, K.
 Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, Y., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishi, K., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Osato, N., Oka, Y., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sugabe, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Waki, K., Yasunishi, A. and Hayashizaki, Y.

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KW protein identification; signal transduction pathway; metabolic pathway;
KW Promoter; termination sequence; ss.
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PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
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PR 28-OCT-1999; 99US-0161920P.
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PR 29-OCT-1999; 99US-0162143P.

Query Match 44.3%; Score 755.8; DB 3; Length 1506;
Best Local Similarity 71.7%; Pred. No. 6.5e-146;
Matches 1036; Conservative 0; Mismatches 397; Indels 12; Gaps 3;
136 ACGCCTCGCGCGGCTCCTTATCTCGGCAATTCGCGCGCTGACAGCAAGTTTCG 195

Db 44 ATGCCACGGCGCGGCGCAACTACATCTGTGCCAGTTAGCGAGCTCAACAACAAATTTA 103
QY 196 TCGACAGGCTTCGCGCTCGACAAACACCTACCTCTCTTTTCGGCTACCTCGTTT 255
Db 104 TCGACAGGCTTCGCTATAGACAAACATACCTCTCTCTTCGGCTACCTCGTTT 163
QY 256 CTATGCAGCTCGGCTTCGCAATCTCTGCGCGGCTCCGTCCGCGCAAGAACACCATGA 315
Db 164 CTATGCAGCTTCGCTTCGCTATGCTCTGTGCCGTTCCGTGAGAGCAAGATACTATGA 223
QY 316 ACATCATGCTCACCAAGCTCTCGAGAGCTCGCGCGCGGCGCTCTTCTACTACCTTCG 375
Db 224 ACATCATGCTTACCAAGCTCTTCGAGCTCGAGCGGCTGCTCTCTTATATATCTGTTG 283
QY 376 GCTTCGCTTCGCTTCGCTCCCTCCCAAGGCTTCATCGGTAAACAATTTCTTCGGCC 435
Db 284 GCTACGCTTCGCTTCGCTTCGATCTCCGTCAATGTTTCATCGGTAAACAATTTCTGTC 343
QY 436 TCAAGGACATCCCTTCATCTCTAGACTACAGTACTTCTCTACCAATGGGCTTCG 495
Db 344 TCAAGACATCCCTCACGCTCTGCTGACTACTTCAACACTTCTCTACCAATGGGCTTCG 403
QY 496 CCATCGCGCGCGCGCATCCAGCGGAAGCATCGCCGAAACGACACACAGTTTCGTGGCT 555
Db 404 CAATCGCTCGCGCTGGAATCACAAAGTGGCTCGATCGTGAACGACACAGTTTCGTGGCT 463
QY 556 ATCTCATCTACTCTCTCTCTCTCACCGGCTTCGTATCCGCTGGTCTCCACTGGTCT 615
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Db 524 GGTCAAGTTGATGATGGGCTGCGGCGGCTTCGATACCGATGGAGATTTGCTTTTCAGACCG 583
QY 673 GCGTAAATAGACTTCGCGGTTTCGGGTTAGTCCACATGTCGCGGGAATAGCCGCTAT 732
Db 584 GAGCGATAGATTTGCTGGGTCGGTGTGTTTATATGTCGAGGTATCGCTGACTCT 643
QY 733 GGGGAGCGCTGATCGAAGCCCAAGATGGGACGTTTCGATCATCGAGAGAGCTGG 792
Db 644 GGGTGGCTCATCGAAGTCCACAGCTTGGCGGTTGATAACGAGAGCGCTGCATCG 703
QY 793 CTTTCGAGGCGACAGCGCTCTTAGTAGTCTCGGAACTCTTTGTTGTTGTTGTTGTT 852
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QY 853 GGTACGATTTTAAACCCCGCTTCAATTAACAATCCTACTTACTTACGTAACAGGAA 912
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QY 973 CAACAGCTGCTTACCAAGCTTATTCGTTAAACGGGTATATCCGCTACCTGAGACGTA 1032
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QY 1033 CCGATGCTGCAACCGGCTTGTAGCGGCTTTTCGGGCGATTAACAGCGGCTTCTCCGTTG 1092
Db 941 CTGATGATGCAACCGGCTCTTCGAGGGTTTTCAGCCATTAACCTGGTGGCTGCTCTGTCG 1000
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Db 1061 ACAAGCTGCTGAGAAGCTCAATACGACGACCTCTTTGAGCGAGCACAACTACACGGTG 1120
QY 1213 GGTGTGGACGCTGGGGGCTGATATTCAGCGGTTGTTTCGCAAAAAGAGTATGTGAAG 1272
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QY 1387 GACCTTGTGTTGGGGTTGAATAAAGCTGTTGAGGATTTCTTCAGAGGATGAGC 1446
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QY 1301 GGACACTTTTCTTCATCCTCAAGAAATGAAATGTTGCGATATCGTCCGAGGATGAGA 1360
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QY 1447 TTGGGGGATGACATGATCGCATGAGGCTTGGTTATGCTTATGAGGATGATGAGA 1506
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QY 1361 TGGCGGTATGATATGACACGGCAGCGTGTGTTGCTTATATGATGTTGATGATG 1420
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QY 1507 CGCAAGCATGGGATGAGTGAAGGAGGTTGGGCCCAACGCTTCCACACCCACCA 1566
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QY 1421 AGTCTCAAGGACATTGAGCTTAGGAGAGTTGAGCCAGCATCTCTTCTCTGTTG 1480
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DB |||||

RESULT 4

ID ABZ13398 standard; DNA; 1506 BP.
XX ABZ13398
AC ABZ13398;
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DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1203.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX
PN WO200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US026685.
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PR 24-AUG-2000; 2000US-0227866P.
XX
PR 26-JAN-2001; 2001US-0264647P.
XX
PR 22-JUN-2001; 2001US-0300111P.
XX
XX (SCRI) SCRIPPS RES INST.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Harper JF, Kreps J, Wang X, Zhu T;
XX
XX WPI; 2002-304127/34.
XX

Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
Claim 144; SEQ ID NO 1203; 577pp + Sequence Listing; English.
The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence

CC information supplied to Derwent by the European Patent Office
XX
SQ Sequence 1506 BP; 307 A; 404 C; 388 G; 407 T; 0 U; 0 Other;
Query Match 44.3%; Score 755.8; DB 6; Length 1506;
Best Local Similarity 71.7%; Pred. No. 6.5e-146;
Matches 1036; Conservative 0; Mismatches 397; Indels 12; Gaps 3;
QY 136 ACCTCTCCGCGCGCTCCCTTATCTGCGGCCAATTCGCGCCGTGGACAGCAAGTTG 195
DB |||||
QY 44 ATGCCACGGCGGCGCAACTACATCTGTGGCCAGTTAGGCGAGCTCAACAACAAATTA 103
DB |||||
QY 196 TCACACGGCTTCGCGCTGCGACACACTACTCTCTTTTCGCGCTACCTGTTTTT 255
DB |||||
QY 104 TCACACGGCTTCGCTATAGACAACTTACTTCTCTCTCGCGCTACCTGTTCTT 163
DB |||||
QY 256 CTATGAGCTTCGCGCTTCGCACTCTGCGCGGCTCGCTCGCGCCCAAGAACCACTGA 315
DB |||||
QY 164 CTATGAGCTTCGCTTCGCTATGCTCTGTGCGGTTCTGAGAGCCAAAGTAATACTA 223
DB |||||
QY 316 ACATCATCTACCAACGCTTCGAGCGCTGCGCGCGGCTCTTCTTACTACCTCTTCT 375
DB |||||
QY 224 ACATCATCTTACCAACGCTTCGAGCTGCGCGCGGTTCTCTTCTTATATCTGTTG 283
DB |||||
QY 376 GCTTCGCTTCGCTTCGCGCTCCCTCCCAACGCTTCATCGGTAAACATTTCTTCGGCC 435
DB |||||
QY 284 GCTTCGCTTCGCTTCGCTCCCTCCCAACGCTTCATCGGTAAACACTACTTTGGTC 343
DB |||||
QY 436 TCAAGGACATCCCTTCATCTCTCTAGGACTACAGTACTTCTCTACCAATGGGCTTCG 495
DB |||||
QY 344 TCAAGGACATCCCAACGCGCTCTGCTGACTACTCAACTTTCTTACCAATGGGCTTCG 403
DB |||||
QY 496 CCATCGCGCGCGGCTTCACGAGGAGCATCGCGGAAAGCATCGCGGAAACAGTTCGTTGG 555
DB |||||
QY 404 CATTCGCTGGGCTGGATCACAAGTGGCTCGATCGTGAACGACAGTTCGTTGGCT 463
DB |||||
QY 556 ATCTCATCTCTCTCTCTCTCACCGGTTGCTATTCGCGGTGGTCTCCACCTGTTCT 615
DB |||||
QY 464 ACCTAATCTATCTCTCTCTTAAACCGGTTGTTTACCGGCTGCTCTCTCACTGGTT 523
DB |||||
QY 616 GGTCCCGCAGCGCTGGGCTCTGCTT---TAAGATCACCGACCGGCTATTTTCCACCG 672
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DB |||||
QY 1033 CCGATGCTTCGAACCGGCTTGTAGCGGTTTTCGCGGGAATAACAACCGGTTGCTCCGTTG 1092
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QY 941 CTGATGATGCAACCGCTCTCTCGAGGGTTTTCGAGCAATACCTGTTGGTCTCTCTCG 1000
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Db 1421 AGTCTCACAAGCCATTCAGCTTAGGAGAGTTGAGCCACGATCTCTTCTCTCTCTG 1480
QY 1567 CTGAT 1571
Db 1481 CTAAT 1485

RESULT 5

AAAC44852
ID AAC44852 standard; DNA; 1572 BP.
XX AC AAC44852;
XX AC AAC44852;
DT 18-OCT-2000 (first entry)
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 44374.
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
KW promoter; termination sequence; ss.

Arabidopsis thaliana.

XX EP1033405-A2.
XX 06-SEP-2000.
XX 25-FEB-2000; 2000EP-00301439.
XX 25-FEB-1999; 99US-0121825P.
XX 05-MAR-1999; 99US-0123180P.
XX 09-MAR-1999; 99US-0123548P.
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PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 44.3%; Score 755.8; DB 3; Length 1572;

Best Local Similarity 71.7%; Pred. No. 6.5e-146;

Matches 1036; Conservative 0; Mismatches 397; Indels 12; Gaps 3;

QY 136 ACGCCCTCCGCGCGCCTCCCTTATCTGCGCCATTCGCGCCCTGGACAGCAAGTTTCG 195
DB 83 ATGCCACGCGCGCGCCAACTACATCTGTGGCCAGTTAGGCGACGTCACCAACAATTTA 142
QY 196 TCGACACGCGCTTCGCGCGCGACACACCTACTCCTCTTTTCGCGCTACCTCGTTTTTT 255
DB 143 TCGACACGCGCTTCGCTATAGACACACTTACTCTCTTTTCGCGCTACCTGTCCTCT 202
QY 256 CTATGCACTCGGCTTCGCGCTCTGCGCGGTCGCTCGCGCCCAAGAACCACTATGA 315
DB 203 CTATGCACTTCGCTTCGCTATGCTCTGTGCGGTTCCGTGAGAGCCAAATACTATGA 262
QY 316 ACATCATGCTACCAACGCTCGGAGCGTGGCGCGCGGCTCTTCTACTACTCTTCG 375
DB 263 ACATCATGCTTACCAACGCTTCGCTGAGCGTGGCGCGGCTCTTCTATCTCTGTTG 322
QY 376 GCTTCGCTTCGCTTCGCGCTCCCTCCAAAGGCTTCATCGGTAAACATTTCTTCGCGC 435
DB 323 GCTACGCTTCGCTTCGCTTCGATCTCGTCCAAATGTTTCATCGGTAAACACTACTTGGTC 382
QY 436 TCAAGGACATCCCTTCATCTCTAGCTACAGTACTTCTCTACCAATGGGCTTCG 495
DB 383 TCAAGACATCCCGCGGCTCTGCTGACTACTCTCACTTTCTTACCAATGGGCTTCG 442
QY 496 CCATCGCGCGCGCGCATCACAGCGGAAGCATCGCGGAACGACACAGTTCGTTGGCT 555
DB 443 CAATCGCTCGGCTCGAATCACAGTGGCTCGATCGCTGAACGACACAGTTCGTTGGCT 502
QY 556 ATCTCATCTCTCTCTCTCTCACGCGCTTCGCTATCCGCTGGTCTCCACCTGGTCT 615
DB 503 ACCTAATCTATTCCTTTCTTAAACGGGTTGTTTACCCTGCTCTCTCTCACTGGTCT 562
QY 616 GGTCCCGACAGCGCTGGGCTCTGCTT---TAAGATCACCGACCGCTATTTTCCACCG 672
DB 563 GGTCACTGATGATGGGCGCGCGCTTCGCTACCGATGGAGATTTGCTTTTCAGACCG 622
QY 673 GCGTATAGACTTCGCGCGGTTCCGCGTAGTCCACATGCTCGCGGGAATAGCGCGCTAT 732
DB 623 GAGCGATAGATTTCCGCTGGGTCGCGTGTGTTTCATATGTCGAGGATTCGCTGACTCT 682
QY 733 GGGGAGCGCTGATCGAAGCCCAAGATGGACGCTTCGATCATGCGAGGACGCTGCG 792
DB 683 GGGTGGCTCATCGAAGTCCACGACTTGGCGGTTTCGATTAACGAGGCGCTGCCATCG 742
QY 793 CCTTGGAGGCGACAGCGGCTTCGCTAGTTCCTGGGAACCTTCTTCTTGGTTCGGT 852
DB 743 CTCTTCGTCGCGCACTCGCGGCTCACTTGTGTCCTTGGAACTTCTCTCTGTTGGAT 802
QY 853 GGTACGGATTTAAACCCCGGTTCAATTAACAAATCTTACTTACGTAACCTACAGAA 912


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Db      803  GGTACGGATTTAAACCCGGTTCCTTCAACAGATCCTAGTACGTACGAGA---CAGGCA 859
QY      913  ATTACTAGGTCATAGGAGCGGTTGSCAGAACGGGGTCCACACTACCTAGCGGGGT 972
Db      860  CATACAAAGCCAGTGGAGCGGTCGACGAGCAGCTGTACACAAACGTTAGCTGGCT 919
QY      973  CAACAGCTGCCTTGACCAACGCTATTCCGTAACCGGGTGATATCCGTCACCTGGAACGTGA 1032
Db      920  GCACCGCGCGCTGACAAACCTATTGGGAACGCTACTCTCGGACATGGGAACGTCA 979
QY     1033  CGGATGCTGCAACCGGCTGTAGCGGTTTCGGCGGATTAACAGCGGGTTGTCCTGGTG 1092
Db      980  CTGATGTATGCAACGGCCCTCTCGAGGGTTTCAGCCATAACTGTGTGGCTGCTCTGTG 1039
QY     1093  TTGAGCCATGGCGACCATCTATGCGGTTTGTGTTCTTATAGTATTAATAGCTTGA 1152
Db     1040  TTGAGCCATGGCTGCGATCATCTGCGGTTCTGCGGCGCCTAGTCCCTCCGATGA 1099
QY     1153  ACAATATTAGCAGAGAGTTAAGTTTCAGCATCTCTGGAGCGGCGCATGTTGCACGGTG 1212
Db     1100  ACAAGCTCGTGAGAAGCTCAATACGACGACCCCTTTGAGGCGACACAACTACACGGTG 1159
QY     1213  GGTGTGGCACCTGGGGGTGATATTACGCGTTGTTTCGCAAAAAGGAGTATGTGAAG 1272
Db     1160  GTTGGGTCGCTGGGACTAATTATTCAGGCTCTCTTCGCTCAAGAAAAGTACTTGAAC 1219
QY     1273  AGTTTACGGTTG-----GGGAGGCGCACGGTTGCTCATGGGGGTGGTGGGAAGT 1326
Db     1220  AGATTTACGGCAACAAACCCGGAAGGCCACACGGTTGTTTATGGCGGTGGAGGAAAC 1279
QY     1327  TGTGGGGGCGACGTGATTCAGATTCGTGATTCGTGGTGGTGGTGGTGGTGGTGGTGG 1386
Db     1280  TACTTGGAGCTCAGCTGATTCAGATCTTGTGATCAGGGTGGGTAAGTGGGACATGG 1339
QY     1387  GACCTTGTGTTGGGGTTGAATAAAGTGAAGCTGTGAGGATTTCTCAGAGGATGAGC 1446
Db     1340  GGACACTTTTCTTCATCCTCAAGAAATGAATGTTGCGGATATCGTCCGAGATGAGA 1399
QY     1447  TTGGGGGATGAGCATGACTCGCCATGGAGGCTTTCGTTATGCTATGAGGATGATGAGA 1506
Db     1400  TGGCCGTTATGATATGACGAGCGCGGTGTTGCTTATATGCTTATATGATGATGATG 1459
QY     1507  CGCAAGCATGGATGACGTTGAGGAGGTTGGGCGCCCAACGCTTCTCCACACCCACCA 1566
Db     1460  AGTCTCAAGAGCAATTCAGCTTAGGAGAGTTGAGCCACGATCTCCTTCTCTCTGTTG 1519
QY     1567  CTGAT 1571
Db     1520  CTAAT 1524

```

RESULT 6

AAQ88327

:D AAQ88327 standard; cDNA; 1748 BP.

CX

CX

CX

CX

CX

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04-MAY-1995.

28-OCT-1993; 93DE-043337597.

28-OCT-1993; 93DE-043337597.

(GENB-) INST GENBIOLOGISCHE FORSCHUNG.

Frommer W, Ninnenmann O;

WPI; 1995-171399/23.

P-PSDB; AAR74676.

Plant ammonium transporter DNA in sense or anti-sense orientation -
 useful for transforming cells, esp. plant cells for prodn. of transgenic
 plants with altered nitrogen metabolism.

Claim 3; Page 17-20; 23pp; German.

The ammonium transporter (AT) gene isolated from *Arabidopsis thaliana*
 (AAQ88327) is a preferred AT gene for use in generating transgenic
 plants. AT gene sequences can be incorporated into expression constructs
 in the sense orientation (for expression of translatable mRNA and hence
 synthesis of AT in the transgenic plants) or in the antisense orientation
 (resulting in antisense transcripts which inhibit synthesis of endogenous
 AT in the transgenic plants). Nitrogen metabolism is altered in the
 resulting transgenic plants; the changes in AT activity may also result
 in plants which are suitable for "low input" crop management or which can
 be grown in acid soils. Yeast and bacteria can also be transformed with
 the AT gene

Sequence 1748 BP; 398 A; 427 C; 421 G; 502 T; 0 U; 0 Other;

Query Match 44.3%; Score 755.8; DB 2; Length 1748;

Best Local Similarity 71.7%; Pred. No. 6.7e-146;

Matches 1036; Conservative 0; Mismatches 397; Indels 12; Gaps 3;

QY 136 AGCCTCCGCCCGCCCTCCCTTATCTGCGGCCATTTCCGCGCGTGGACAGCAAGTTTCG 195

Db 64 ATGCCACGCGCGCGCAACTACATATGTGCCAGCTAGGCGAGCTCAACAACTCA 123

QY 196 TCGACACGCGCTTCGCGTGCACACACTACCTCTCTTTTCGCGCTACCTCGTTTTT 255

Db 124 TCGACACGCGCTTCGCTATAGACAACTTACCTCTCTCTTCGCGCTACCTCTCTCT 183

QY 256 CTATGACGCTCGGCTTCGCCATGCTCTCGCGCGTCCGTCGCGCCAGCAACCATGA 315

Db 184 CTATGACGCTTCGCTTCGCTATGCTCTGTCGCGTTCGTCGAGCCAGATATGA 243

QY 316 ACATCATGCTACCAACGCTCTGACGCTGCGCGCGGCGCTTTTCTACTACTCTTCG 375

Db 244 ACATCATGCTTACCAACGCTCTGACGCTGCGCGCGGCTTCGTCGAGCCAGATATGA 303

QY 376 GCTTCGCTTCGCTTCGCGTCCCTCCACGCTTCATCGGTAAACATTTCTTCGCGCC 435

Db 304 GCTACGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTC 363

QY 436 TCAAGGACATCTCTTCATCT 495

Db 364 TCAAGGACATCT 423

QY 496 CCATCGCGCGCGCGCATCACACGCGGAGCATCGCGGAGCAACAGCTTCGCTTCGCGCT 555

Db 424 CAATGCTTCGCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 483

QY 556 ATCTCATCT 615

Db 484 ACCTAATCTATTTCT 543

QY 616 GGTCCCGACGCGCTGCGCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 672

Db 544 GGTCTGATGATGCGGCGCGCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 603

Arabidopsis thaliana ammonium transporter gene.
 Nitrogen metabolism; transgenic plant; ammonium transporter gene;
 antisense; inhibition; low input crop management; ds.

Arabidopsis thaliana.

Key Location/Qualifiers

21..1526

/*tag= a

/product= "Ammonium_transporter"

DB4337597-A1.

Db 422 TCCTTACCAATGGGCTTTTCCCATAGCGCGCGGAATCACTAGCGTTCATCGCG 481
QY 535 AACGACACAGTTCGTGGCCCTATCTCACTACCTCTCTCCACGCGTTCGTCTATC 594
Db 482 AGCGAAGCAATTCGTTCCTTACCTTATCTACTCTTCTTTCGACCGGTTTGTATTAC 541
QY 595 CGGTGCTTCCACATGCTTCTGGTCCCGACAGCGCTGGG-CTCTGCTTTTAAAGTCA 651
Db 542 CGACAGTCTCGCACTGGTCTCTGGTCAAGTATGATGGCTACGCGTCCGCTCTGACA 601
QY 652 CGACCGGCTATTTCCACCGCGGTATAGACTTCGCGGTTCCGCGTAGTCCACATGG 711
Db 602 ACAATCTCTTGTGGTCAAGTATGATGGCTACGCGTTCAGAGTGTTCACATGG 661
QY 712 TCGCGGAATACCGCGCTTATGGGAGCGCTGATCGAAGGCCCAAGATGGGACGTTTCG 771
Db 662 TAGGTGGAATTCGCGGTTTATGTGGAGCGTATGTGAAGGACCAAGATAGGTAGATTG 721
QY 772 ATCATGCGAGGAGCTGTGGCTTGGAGCCACAGCGGCTTATAGTCTCTGGGA 831
Db 722 ACCGTACAGCGGTCGCTGGCTTATCGTGTACAGTGCATCCCTTGTGCTGTGTA 781
QY 832 CTTCTTCTTGTGTGGTGTGACGATTTAAACCCGCTTCAITTAACAAATCCTAC 891
Db 782 CTTCTTGTGTGGTGTGATGTGTGGTATGCGTTCCTTTTAAACATCTTA 841
QY 892 TTAATGAGGTAATCACTAGGAATTAAGTACGTCAGTGCAGCGGTTGACAGCGGG 951
Db 842 AAGGTACGACAGTCTCGGCAATATTATGTCAATGAGCGCTGAGTGCAGCGGG 901
QY 952 TCACCACTACCTAGCGGGTCAACAGCTGCTTGCACGCTATTCGTTAAACGGTGA 1011
Db 902 TCACCACTACCTAGCGGGTCAACAGCTGCTTGCACGCTATTCGTTAAACGGCTT 961
QY 1012 TATCGGTCACTGGAACGCTGATCTGACAGCGGCTTATAGCGGTTTCGCGGA 1071
Db 962 TAGCAGGTCATGGAACGTTTATGACGTATGACAGGCTTATAGCGGCTTTCAGCTA 1021
QY 1072 TAAACCGCGTGTCTCCGTTGAGCCATGCGCAGCATCGTATCGGTTTGTGCTT 1131
Db 1022 TAACTCCGATGTCCGCTGCGGAGCGCTGCTATAGTATGTGCTTGTGGCAT 1081
QY 1132 CTATAGTATTAAGTTCGCAAAATAGCAGAGGTTAAGTTCGAGCTCTCTGG 1191
Db 1082 CATGGTTTATTCGATTTAATCTGCTTGCACAAACTTAATATGATGACCACTG 1141
QY 1192 AGCGCGCGAGTTCACGCTGGGTGTGCGACGTGGGGGTGATTAATCACGGCTTGTTCG 1251
Db 1142 AGCGCTGCTCAGCTCCAGCTGATGTGAGCATGGGATTAATCTTTACGGGCTGTTG 1201
QY 1252 CAAAAGGAGTATGAGGAGGTTTACGGTTGGGAGGCGCAGCGGTTGCTCATGG 1311
Db 1202 CAAAGAAAGATACGTTAAACAGATTTTACTCCGCTGATAGGCTTACGAGCTGTTATGG 1261
QY 1312 GGGGTGTGGGAAGTGTGTCGCGCGCACGTTGATTCAGATTCGTGATTCGTGGGTGG 1371
Db 1262 GCGGGGAGGAAACTGCTCCGCGCGAGATCGTTTCAAGATTTATGTGATCGTTGGGTGG 1321
QY 1372 TTAGTGCAGCAGGAGGCTTGTGTTGGGGTTGATTAATCACTGAAGCTGTGAGGATTT 1431
Db 1322 TGACGGTAACTATGGGACCGTTGTTTATGGGTTTACATAGATGATCTTTTGGAGATAT 1381
QY 1432 CTTTACAGATGAGCTTCGCGGAGTGAATGATCGCCATGAGGCTTGTCTTATGCTT 1491
Db 1382 CAGCAGAGATGAGATGGCAGGATGACATGACACGCTCATGGAGGATTTGTTACGGAT 1441
QY 1492 ATGAGGATGATCA 1504
Db 1442 ACAAAGCAGAGA 1454

RESULT 8

ABZ14082
ID ABZ14082 standard; DNA; 1497 BP.
XX
AC ABZ14082;
XX
DT 21-JAN-2003 (first entry)
XX
DE Arabidopsis thaliana stress regulated gene SEQ ID NO 1887.
XX
KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.
XX
OS Arabidopsis thaliana.
XX
PN W0200216655-A2.
XX
PD 28-FEB-2002.
XX
PF 24-AUG-2001; 2001WO-US026685.
XX
PR 24-AUG-2000; 2000US-0227866P.
PR 28-JAN-2001; 2001US-0264647P.
PR 22-JUN-2001; 2001US-0300111P.
XX
(SCRI) SCRIPES RES INST.
(SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Harper JF, Krops J, Wang X, Zhu T;
XX
WI; 2002-304127/34.
XX
Identifying a stress condition to which a plant cell has been exposed and
producing plants with increased tolerance to these abiotic stresses.
XX
Claim 144; SEQ ID NO 1887; 577pp + Sequence Listing; English.
XX
The invention relates to identifying a stress condition to which a plant
cell has been exposed, comprising: (a) contacting nucleic acid
representative of expressed polynucleotides in the plant cell with an
array or probes representative of the plant cell genome; and (b)
detecting a profile of expressed polynucleotides in the plant cell
characteristic of a stress response. The method is useful in the
production of transgenic plants, cells and seeds and in producing plants
with increased tolerance to abiotic stress. The present sequence is that
of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used
in methods of the invention. Note: The sequence data for this patent is
not represented in the printed specification but is based on sequence
information supplied to Derwent by the European Patent Office
XX
SQ Sequence 1497 BP; 309 A; 386 C; 385 G; 417 T; 0 U; 0 Other;

Query Match 41.1%; Score 700.4; DB 6; Length 1497;
Best Local Similarity 69.7%; Pred. No. 1.6e-134;
Matches 995; Conservative 0; Mismatches 421; Indels 12; Gaps 3;
QY 107 GGGCCAACTTCGGGCCCAACACACAGAGCGCTCGCGCGCGCTCCCTTATCTGCGG 166
Db 27 GCGCATCTCGCACCTTACTTGGCCCAACAGCCACGCGCGCGCGCTTACATTTGCGG 86
QY 167 CCATTTTCGCGCGCGTGGACAGAGTTCTGACACAGCGCTTCGCGCTCGACAACTTA 226
Db 87 CCATTTAGCACCTTACACACAGTTTCCCGATGACGCTTCGCCATAGACACACTTA 146
QY 227 CTTCTCTTTTTCGCGCTACCTCGCTTTTCTATGACGCTCGGCTTCGCCATGCTGCGC 286
Db 147 CTTCTCTTTTCTGCTACCTTGTCTTTCGCGCATGACGCTCGGCTTCGCTATGCTTGTG 206
QY 287 CGGCTCGGTCGCGCGCAAGAACACCATGAACATCATGCTCACCAGGCTTCCTGACGCTGC 346
Db 207 TGGTCTGTAGGCCAAGATACGATGACATCATCTTACCAATGCTCTTTCGCGCTGC 266
QY 347 CGCGCGCGGCTCTTCTACTACTCTTTCGCGCTTCGCGCTTCGCTTCGCTTCGCCCTCCA 406
Db 267 AGCGGAGGACTCTTCTACTATCTCTTGTGTTACGCTTTTGCCTTTGGAGGATCTCCGA 326

KX	De	Oligonucleotide for detecting cytosine methylation SEQ ID NO 31407.
KX	De	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW	KW	drug; side effect; cancer; central nervous system; cardiovascular;
KW	KW	gastrointestinal; respiratory system; single nucleotide polymorphism;
KW	KW	SNP; cell differentiation; ds.
DS	DS	Homo sapiens.
PN	PN	WO200218632-A2.
CX	CX	07-MAR-2002.
PD	PD	01-SEP-2001; 2001WO-EP010074.
PF	PF	01-SEP-2000; 2000DE-01043826.
PR	PR	05-SEP-2000; 2000DE-01044543.
PS	PS	(EPIG-) EPIGENOMICS AG.
PA	PA	Olek A, Piepenbrock C, Berlin K, Guetig D;
PI	PI	WPI; 2002-371829/40.
PR	PR	Determining the degree of cytosine methylation in genomic DNA, useful for
PT	PT	diagnosis and prognosis, comprises selective hybridization of amplicons
PT	PT	from chemically treated DNA.
CX	CX	Claim 12; 56pp + Sequence Listing; 56pp; German.
CS	CS	This invention describes a novel method for determining the degree of
CC	CC	methylation of a particular cytosine in a motif 5'-CPG-3', present in a
CC	CC	genomic sample of DNA. The sample is treated chemically to convert
CC	CC	cytosine (C) but not methylated C, to uracil, then part of the genomic
CC	CC	DNA that contains the target C is amplified to form a labeled amplicon.
CC	CC	The amplicon is hybridised to two classes, each with at least one member,
CC	CC	of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the
CC	CC	degree of hybridisation to both classes is determined from the label on
CC	CC	the amplicon. From the ratio of labels hybridised to the two classes of
CC	CC	oligomers, the degree of methylation is calculated. The method is used:
CC	CC	(i) for diagnosis and/or prognosis of side effects of therapeutic drugs
CC	CC	and of a wide range of diseases, e.g. cancer, disorders of the central
CC	CC	nervous, cardiovascular, gastrointestinal and respiratory systems etc.,
CC	CC	particularly by detecting mutations or single nucleotide polymorphisms
CC	CC	(SNP's); and (ii) for differentiation of cell or tissue types and for
CC	CC	investigating cell differentiation. The method allows the methylation
CC	CC	status of many C residues to be determined simultaneously. ABQ13410-
CC	CC	ABQ54121 represent genomic DNA sequences used to illustrate the method
CC	CC	for determining the degree of cytosine methylation described in the
CC	CC	disclosure of the invention
KX	KX	Sequence 995 BP; 234 A; 145 C; 326 G; 280 T; 0 U; 0 Other;
SQ	SQ	Query Match 5.2%; Score 89; DB 6; Length 985;
		Best Local Similarity 49.7%; Pred.No. 1.1e-08;
		Matches 227; Conservative 0; Mismatches 230; Indels 0; Gaps 0
2Y	2Y	136 AGCCTCCGCGCGCTCCCTTATCTCGGCAATTCGCGCGCTGGACGACGAGTTGG 195
2b	2b	600 ACATCGAGTGCATCTACGTCAAGCTCAAGCTGACATCGACGTCGACATCTACGTCG 541
2Y	2Y	196 TGCACACGGCTTCGGCGTCGACACACCTACCTCTCTTTTCGGCTACCTCGTTTTT 255
2b	2b	540 AGCTCTACATCTAGCTCGACGTCGACGCTTACATCTACGTCTACATCAACATCAATCT 481
2Y	2Y	256 CTATGACGCTCGGCTTCGCCATGCTCTCGCGCGGCTCCGTCGGCGGACAGACACATGA 315
2b	2b	480 ACATCTACATCTAGTGCAGCTTACATCTACGTGACATCTACGTCTACATCTAGCTCT 421
2Y	2Y	316 ACATCATGCTCACCAAGTCTCTGGACGCTCGCGCGCGGCTCTTTCTACTACCTCTTCG 375
2b	2b	420 ACATCTAGCTCTACATCTACGTCAAGCTGACGTCGACGTCGACATCTACGTTCGACATCT 361

CC	AB054121	represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention
CC		
CC		
XX		
SQ	Sequence 985 BP; 280 A; 326 C; 145 G; 234 T; 0 U; 0 Other;	
	Query Match	5.2%; Score 89; DB 6; Length 985;
	Best Local Similarity	49.7%; Pred. No. 1.1e-08;
	Matches 227; Conservative	0; Mismatches 230; Indels 0; Gaps 0
QY	136	ACGCTTCGCGCGCGCTCCCTTATCTGCGGCATTTGCGCGCGTGGACAGCAAGTTGCG 195
DB	386	ACATCGACGTCGACATCTACGTCACAGTCACGATCGATCGATCTTACGTCG 445
QY	196	TCGACACGGCCTTCGCGTCGACACACGCTACCTCTCTTTTCGCGCTACCTGTTTTT 255
DB	446	ACGCTTACATCTACGTCGACGTCGACGCTTACATCTACGCTACATCAACATCATCT 505
QY	256	CTATGCAGCTCGCGCTTCGCGCATGCTCTGCGCGGCTCGCTCGGCGCAAGAACACCATGA 315
DB	506	ACATCTACATCTACGTCGACGCTTACATCTACGTCGACATCTAGCTCTACATCTAGCTCT 565
QY	316	ACATCATGCTACACAGCTCTGAGCGTGCAGCGTGCAGCGCGCGGCTTTCTTACTACTCTTCG 375
DB	566	ACATCTACGCTCTACATCTACGTCACAGTCGACGTCGACGTCGACATCTACGTCGACATCT 625
QY	376	GGTTTCGCTTCGCTTTTCGGCTCCCTCCACCGCTTCATCGGTAACATTTCTTCGGCC 435
DB	626	ACGTCGACATCGACATCGACATCGACATCGACGTCGACGTCGACATCTACGTCGACATCT 685
QY	436	TCAAGACATCCCTTCATCTCTTCAGACTACAGCTACTTCTCTTACCAATGGGCGCTTCG 495
DB	686	ACGCTCTACATCTACGTCGACATCTACGTCACAGTCACAGTCGACATCTACGTCACAGTCG 745
QY	496	CCATCGCGCGCGCGCATCCAGCGGAGCATCGCGGAGCATCGCGGACGACACAGTTGCTGGCT 555
DB	746	ACATCGACATCAAGTCGACATCGACATCAACATCTACGTCGACATCTACGTCGACATCT 805
QY	556	ATCTCATCTACTTCCTTCCTTCCTCAGCGCTTCGTCCTA 592
DB	806	ACGCTCTACATCAACATCAACATCAACATCTACGTCGACGCTA 842
RESULT 13		
ABE11211		
ID	ABE11211	standard; cDNA; 1956 BP.
AC	ABE11211;	
XX		
XX		
DT	26-MAR-2002	(first entry)
XX		
DE	Drosophila melanogaster	expressed polynucleotide SEQ ID NO 28115.
XX		
KW	Drosophila;	developmental biology; cell signalling; insecticide;
KW	pharmaceutical;	gene; ss.
XX		
OS	Drosophila melanogaster.	
XX		
PN	WO200171042-A2.	
XX		
PD	27-SEP-2001.	
XX		
PF	23-MAR-2001;	2001WO-US009231.
XX		
PR	23-MAR-2000;	2000US-0191637P.
PR	11-JUL-2000;	2000US-00614150.
XX		
PA	(PEKE)	PE CORP NY.
XX		
PI	Venter JC, Adams M, Li PWD,	Myers EW;
XX		
DR	WPI;	2001-656860/75.
DR	P-PsDB;	ABE67108.

XX	PT	New isolated nucleic acid detection reagent for detecting 1000 or more
XX	PT	genes from Drosophila and for elucidating cell signaling and cell-cell
XX	PT	interactions.
PS	PS	Claim 1; SEQ ID NO 28115; 21pp + Sequence Listing; English.
XX	CC	The invention relates to an isolated nucleic acid detection reagent
XX	CC	capable of detecting 1000 or more genes from Drosophila. The invention is
XX	CC	useful in developmental biology and in elucidating cell signaling and
XX	CC	cell-cell interactions in higher eukaryotes for the development of
XX	CC	insecticides, therapeutics and pharmaceutical drugs. The invention
XX	CC	discloses genomic DNA sequences (ABL161176-ABL30511), expressed DNA
XX	CC	sequences (ABL01840-ABL161175) and the encoded proteins (AB857737-
XX	CC	AB872072). The sequence data for this patent did not form part of the
XX	CC	printed specification, but was obtained in electronic format directly
XX	CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ	SQ	Sequence 1956 BP; 395 A; 536 C; 549 G; 476 T; 0 U; 0 Other;
<p>Query Match 5.1%; Score 87.6; DB 4; Length 1956;</p> <p>Best Local Similarity 55.6%; Pred. No. 2.4e-08;</p> <p>Matches 218; Conservative 0; Mismatches 159; Indels 15; Gaps 2</p>		
Qy	206	CTTCGCGCTCGACAACACTACTCTCTTTTCGCGCTACTCGTGTCTTTTCTATGCAGCT 265
Db	336	CTCCGTCGAGGACACCAACTGGTCTCTCTCTTCATCATCTTCACCAATGCAAC 395
Qy	266	CGGCTTCGCGCATGCTCTCGCGCGGCTCGTCGCGGCCAAGAACACCATGAACATCATGCT 325
Db	396	GGGTTTCGGTATGCTGGAGTCCGGTTGTGAAGCATCAAGACGAGGTGAACATCATGAT 455
Qy	326	CACCAACGTCCTGGAGCGCTGCGCGCGCGCTCTTCTACTACTCTCTCGGCTTCG --- 381
Db	456	GAAGAACGTGATGCACATTTCTGGCGGATTTACTTCTGCTCTTCGGTACGGAAAT 515
Qy	382	--CCTTCGCTTTTCGGCTCCCTCCCAAGCGCTTCATCGGTAACATTTCTTCGGCTCA 439
Db	516	GAGCTTCGGTCGCGGCCCACTCTCCATTCATTCGCGCACTTCCTGCTGGA 575
Qy	440	-----GGACATCCCTTCATCTCTCTACGACTACAGTACTTCTCTACCAATGGCG 490
Db	576	TCACGGTGGCGATGACATGATGGACAGATTTTTCGCGCTCTCTGTTCCAACTGTC 635
Qy	491	CTTCGCCATCGCCGCGCGCATCACACGGAAGCATCGCGCAACGACACATGTTGCT 550
Db	636	GTTTCGCCACCGGCCACACCAATGTTCAGCGCGCATGGCTGAACGTGCACTTTAA 695
Qy	551	GGCTATCTCATCTACT 582
Db	696	GGCATACTGCTGTCT 727
<p>RESULT 14</p> <p>AAD07130/c</p> <p>ID AAD07130 standard; cDNA; 2805 BP.</p> <p>XX AAD07130;</p> <p>AC</p> <p>XX</p> <p>DT 06-AUG-2001 (first entry)</p> <p>XX</p> <p>XX</p> <p>DE Canine retinitis pigmentosa GTPase regulator (RPGR) cDNA.</p> <p>XX</p> <p>XX Dog; X-linked progressive retinal atrophy; XLPRA; genetic marker;</p> <p>XX retinitis pigmentosa GTPase regulator; RPGR; Siberian Husky; Samoyed;</p> <p>KW Miniature Schnauzer; ss.</p> <p>XX</p> <p>XX Canis familiaris.</p> <p>OS</p> <p>XX</p> <p>XX</p> <p>Key Location/Qualifiers</p> <p>PH 1.1569</p> <p>FT /*tag= a</p> <p>FT /product= "Canine retinitis pigmentosa GTPase regulator"</p> <p>FT</p>		

/note= "CDS does not include start codon"
/partial

FT WO200138578-A1.
XX 31-MAY-2001.
XX 21-NOV-2000; 200WO-US031940.
XX 24-NOV-1999; 99US-0167365P.
XX (CORR) CORNELL RES FOUND INC.
XX Aguirre GD, Acland GM, Zhang Q, Ray K, Zeiss CJ;
XX WPI; 2001-367707/38.
XX P-PSDB; AAE02397.
XX Identifying dogs with or carrying X-linked progressive retinal atrophy by
XX detecting retinitis pigmentosa GTPase regulator gene mutation, useful
XX when breeding Husky, Samoyed and Miniature Schnauzer.
XX Claim 71; Page 30-31; 88pp; English.
XX The invention relates to a method for identifying dogs which are
XX genetically normal, are carriers of, or are affected with X-linked
XX progressive retinal atrophy (XLPRA), by testing a biological sample with
XX genetic markers that co-segregate with a XLPRA gene locus. The invention
XX also relates to canine retinitis pigmentosa GTPase regulator (RPGR), RPGR
XX mutants and their corresponding nucleic acid molecules. The mutated RPGR
XX genes are responsible for the XLPRA in dogs. Methods are used to select
XX dogs for breeding so that dogs carrying the mutated locus are eliminated
XX from the breeding stock. The method particularly applies to Siberian
XX Husky, Samoyed and Miniature Schnauzer breeds, or any other breed where
XX the disease is X-linked. XLPRA1 type is identified in Siberian Huskies,
XX and Samoyeds, while XLPRA2 type is identified in Miniature Schnauzers.
XX The present cDNA sequence is the normal open reading frame (ORF) 15
XX encoding canine retinitis pigmentosa GTPase regulator (RPGR) protein
XX found in normal dogs
XX Sequence 2805 BP; 1029 A; 287 C; 940 G; 549 T; 0 U; 0 Other;
XX
XX Query Match 5.0%; Score 85.2; DB 4; Length 2805;
XX Best Local Similarity 46.8%; Pred. No. 8.3e-08;
XX Matches 267; Conservative 0; Mismatches 303; Indels 0; Gaps 0;
XX
QY 137 CGCTCCGCGCGCCCTCCCTTATCTGCGCCATTTTCGCGCGCGGAGCAGCAAGTTGGT 196
Db 1123 CCCCT 1064
QY 197 CGACAGCGCTTCGCGTGCAGACACCTACTCTCTCTCTCTCTCTCTCTCTCTCTCT 256
Db 1063 CTTCT 1004
QY 257 TATGACGTGGCTTCGCCATGTCTGCGCGGCTCGTCCGCGGCAAGAACACCATGAA 316
Db 1003 CTTCTGCGCTGTCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 944
QY 317 CATCATGCTACCAAGCTCTGAGCGTGGCGGCGGCGGCTCTCTCTCTCTCTCTCTCT 376
Db 943 CTTCT 884
QY 377 CTTGCGCTTCGCTTCGGCTTCGCGTCCAGCGGCTTCATCGGTAACATTTCTTCGGCT 436
Db 883 ATTCTCTTTGTTTCT 824
QY 437 CAAGGACATCCCTTCATCT 496
Db 823 CATCT 764
QY 497 CATCGCGCGCGCGGATCATCCAGCGGAGCATGCGCGGAGCAGACACAGTTCGTGGCTA 556
Db 763 CCATCT 704

QY 557 TCTCATCTACTG 616
Db 703 CTTCCCATTTCTGCT 644
QY 617 GTCCCCAGAGCGGTGGGCTCTGCGCTTTAAGATACCGACCGGCTATTTCACGGGCT 676
Db 643 CCCCCT 584
QY 677 AATAGACTTTCGCGGTTTCGGGCTAGTCCA 706
Db 583 CCTCTAATTCCT 554

RESULT 15

ABL11210/c
ID ABL11210 standard; cDNA; 5296 BP.

XX AC ABL11210;
XX 26-MAR-2002 (first entry)
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 28112.
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX Drosophila melanogaster.
XX WO200171042-A2.
XX 27-SEP-2001.
XX 23-MAR-2001; 2001WO-US009231.
XX 23-MAR-2000; 2000US-0191637P.
XX 11-JUL-2000; 2000US-00614150.
XX (PEKE) PE CORP NY.
XX Venter JC, Adams M, Li PWD, Myers EW;
XX WPI; 2001-556860/75.
XX P-PSDB; ABB67107.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signaling and cell-cell
PT interactions.

XX Claim 1; SEQ ID NO 28112; 21pp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7737-
XX ABBS72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 5296 BP; 1425 A; 1165 C; 1199 G; 1507 T; 0 U; 0 Other;

Query Match 4.6%; Score 78.6; DB 4; Length 5296;
Best Local Similarity 54.9%; Pred. No. 2.2e-06;
Matches 206; Conservative 0; Mismatches 154; Indels 15; Gaps 2;

QY 206 CTTGCGCGTGCAGAACACCTACTCTCTCTTTTCGCGCTTACCTCGTTTTTTCATGCACT 265
Db 2823 CTCGTCGAGGACACCAACTGGTCTCTGACCTCTCTCTCTCTCTCTCTCTCTCTCT 2764
QY 266 CGGCTTCGCCATGTCTCTGGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 325

Db	2763	GGTTTCGGTATGCTGGAGTCCGTTGTGTAAGCATCAAGAACGAGTGAACATCATGAT	2704
QY	326	CACCAACGTCCTGGACGCTGCGCGCGGCTCTTCTACTACTCTTGGGCTTCG----	381
Db	2703	GAAGAACGTGATCGACATTGTTCTGGGGGATTTACTTCTGCTCTTGGCTACGGAAT	2644
QY	382	--CCTTCGCTTTCGGCTCCCTCCAAAGGCTTCATCGGTAACATTTCTTGGGCTCAA	439
Db	2643	GAGCTTCGGTCGCGCGCCACTCTCCAAATCCATTCAATGCGCAATGGGGAATTCCTGCTGA	2584
QY	440	-----GGACATCCCTTCATCCTCCTACGACTACAGCTACTTCTTACCAATGGGC	490
Db	2583	TCCACCGTGGCGATGCACTGATGGGACAGATTTTGCCGCTTCTGTTCCACTGTC	2524
QY	491	CTTGCCATCGCCGCGCGGCTACACAGCGAAGCATCGCCGAACGACACAGTTGTT	550
Db	2523	GTTCCGCCACACGCGCCACAAACATTGTACGCGCGCCATGGCTGAACGGTGATACCAT	2464
QY	551	GGCCTATCTCATCTA	565
Db	2463	GATACATCTCTACTA	2449

Search completed: March 9, 2004, 10:48:21
Job time : 758 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2004, 10:35:31 ; Search time 155 Seconds
(without alignments)
6108.040 Million cell updates/sec

Title: US-10-033-109-3
Perfect score: 1706
Sequence: 1 gcacgagcactcccaacccc.....aaaaaaaaaaaaaaaaaaaaa 1706

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5A COMB.seq:
2: /cgn2_6/prodata/2/ina/5B COMB.seq:
3: /cgn2_6/prodata/2/ina/6A COMB.seq:
4: /cgn2_6/prodata/2/ina/6B COMB.seq:
5: /cgn2_6/prodata/2/ina/PCUTS COMB.seq:
6: /cgn2_6/prodata/2/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	ID	Description
1	755.8	44.3	1748	4	US-08-635-967-1
2	91.4	5.4	1926	4	US-09-249-585A-4
3	91.4	5.4	1931	2	US-09-130-114-2
4	82	4.8	7218	1	US-08-232-463-14
5	76.6	4.5	390	3	US-09-197-649-7
6	76	4.5	1926	4	US-09-249-585A-2
7	76	4.5	1926	4	US-09-410-399-3
8	76	4.5	2580	3	US-09-050-863-2
9	76	4.5	2580	4	US-09-359-081-2
10	76	4.5	5452	2	US-09-130-114-1
11	76	4.5	8705	4	US-09-647-344A-14
12	76	4.5	9600	3	US-08-910-647-1
13	76	4.5	9600	4	US-09-620-925-1
14	76	4.5	10596	1	US-07-884-811-15
15	76	4.5	10596	1	US-07-885-971-15
16	76	4.5	10596	1	US-08-087-783A-15
17	76	4.5	10596	1	US-08-194-088B-15
18	76	4.5	10596	2	US-08-194-087-15
19	76	4.5	10596	5	PCT-US93-04648-15
20	76	4.5	16880	4	US-09-724-566A-48
21	74.4	4.4	4403765	3	US-09-103-840A-2
22	74.4	4.4	4411529	3	US-09-103-840A-1
23	74.2	4.3	1248	3	US-09-105-537-7
24	74.2	4.3	13613	3	US-09-105-537-3
25	68	4.0	1505	1	US-07-915-246-1
26	66.6	3.9	5970	3	US-09-320-878-21
27	66.6	3.9	5970	4	US-09-141-908-11

Sequence 21, Appl
Sequence 26, Appl
Sequence 26, Appl
Sequence 208, Appl
Sequence 208, Appl
Sequence 2, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 12, Appl
Sequence 18, Appl
Sequence 1, Appl

ALIGNMENTS

RESULT 1

US-08-635-967-1
; Sequence 1, Application US/08635967
; Patent No. 6620610
; GENERAL INFORMATION:
; APPLICANT: FROMMER, Wolf-Bernd
; APPLICANT: NINNEMAN, Olaf
; TITLE OF INVENTION: DNA SEQUENCES FOR AMMONIUM TRANSPORTER,
; TITLE OF INVENTION: PLASMIDS, BACTERIA, YEASTS, PLANT CELLS AND PLANTS
; TITLE OF INVENTION: CONTAINING THE TRANSPORTER
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen, LLP
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,967
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP 94/03499
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 37 597.9
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Meilman, Edward
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/951-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1748 base pairs
; TYPE: nucleic acid
; TOPOLOGY: single
; STRANDEDNESS: single
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana

INDIVIDUAL ISOLATE: Ammonium transporter

IMMEDIATE SOURCE: CDNA library in plasmid pF161

POSITION IN GENOME: MAP POSITION: from 21 to 1523 coding region

FEATURE: NAME/KEY: CDS

LOCATION: 21...1526

S-08-635-967-1

Query Match 44.3%; Score 755.8; DB 4; Length 1748;

Best Local Similarity 71.7%; Pred. No. 1.7e-173;

Matches 1036; Conservative 0; Mismatches 397; Indels 12; Gaps 3;

Y 136 AGCCCTCCGCGCCGCTCCCTTATCTCGGCAATTTCCGCGCGTGGAGACAGCAAGTTG 195
b 64 ATGCCACGGCGGCGCAACTACATATGTGGCAGCTAGGAGGTCAAACAATTCA 123
Y 196 TCGACACGGCCTTCGCGGTGGAACAACCTACTCTCTTTTTCGCGCTACTCTGTTTTT 255
b 124 TCGACACCGCTTTGCTATAGACAACACTTACTCTCTCTTCTCGCGCTACTCTGTTCT 183
Y 256 CTATGACGCTCGGCTTCGCACTCTCTCGCGGTCTCGCGGCTCGCGGCAAGAACACATGA 315
b 184 CTATGACGCTCGGCTTCGCTATGCTCTCTGCGGTTCGCGAGAGCCAGAACTACTATGA 243
Y 316 ACATCATGCTCAACCAAGCTCTGAGCTCGCGCGGCGCTCTTCTACTACTCTCTG 375
b 244 ACATCATGCTTACCAAGCTCTGAGCTCGCGCGGTCTCTCTTATATCTGTTG 303
Y 376 GCTTGGCTTCGCTTCGCTCCCTCCAGCGGTCTCATCGGTAAACATTTCTTGGCC 435
b 304 GCTACGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTC 363
Y 436 TCAAGACATCCCTTATCTCTCTCACTACAGTACTTCTCTTACCAATGGGCTTCG 495
b 364 TCAAGACATCCCTTATCTCTCTCACTACAGTACTTCTCTTACCAATGGGCTTCG 423
Y 496 CATATCGCGCGCGGCTACCGGGAAGCATCGCGGACGACACAGTTCGTCGCT 555
b 424 CAATCGCTCGGCTGGAATCAAGTGGCTCGATCGCTGAACGACAGTTCGTCGCT 483
Y 556 ATCTCATCTACTCTCTCTCTCTCACGGCTTCTATCTCGGTGCTCTCCACTGTTCT 615
b 484 ACCTATCTATCTCTCTCTCTTAAACGGGTGTTGTTTACCGGTCTCTCTCACTGTTCT 543
Y 616 GGTCCCAAGCGCTGGGCTCTGCTT---TAAGATCACGACGGGTATTTTCACCG 672
b 544 GGTCACTGATGATGGGCGGCGGCTTCCGTACCGATGGAGATTTGCTTTCAGCACCG 603
Y 673 GCGTAATAGACTTCGCGGCTTCGCGGTAGTCCACATGCTCGGCGAATAGCCGCTAT 732
b 604 GAGGATAGATTTGCTGGGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 663
Y 733 GGGGAGCGGTATCGAGAGCCCAAGATGGAGAGTTCGATCATGCGAGGAGCTGTTG 792
b 664 GGGGTGCTATCGAAGGTTCACAGCTTGGCGGTTCGATACGGAAGCGGCTGCCATCG 723
Y 793 CTTTGGAGGACACAGCGGTCTCTAGTCTGCTGGGAACCTTCTTGTGTTGCTCGGT 852
b 724 CTCTTGGGCACTCGGCTCACTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 783
Y 853 GTPACGGATTAACCCGGTTCATTTAACAATCTTACTTACTGTTAGGTAACTCAGAA 912
b 784 GTPACGGATTAACCCGGTTCATTTAACAATCTTACTTACTGTTAGGTAACTCAGAA 840
Y 913 ATTACTACGCTCAATGGAGCGGTGGAGAACCGGTACCACTACCTCTAGCGGGT 972
b 841 CATCAAGCGGCTGAGCGGCTGCGAGCAGCTGTCAACAACGTTAGCTGGCT 900
Y 973 CAACAGCTGCTTACCAAGCTTATGCTGTAACAGGGGTGATATCGGTCACCTGGAACGTGA 1032
b 901 GCACCGCGGCTGACAAACCTTATTTGGAAACGTCTACTCTCGGGAATTTGGAACGTCA 960

QY 1033 CCGATGCTCGAACGGGCTGTTAGGGGTTTCGCGCGGATAACAGCCGTTGCTCGTGG 1092
Db 961 CTGATGATGACACGGCTCTCTCGAGGGTTTCGACCATTAAGTGGTCTGCTCTGTCG 1020
QY 1093 TTGAGCCATGGGCGAGCCATCGTATGCGGTTTGTCTCTATAGTATTAATAGCTTGA 1152
Db 1021 TTGAGCCATGGGCTGCGATCATCTGCGGGTTCGTCGGGCTTCTCTCTCGATGCA 1080
QY 1153 ACAAATTTAGCAGAGAGGTTAAGTTGACGATCTCTGAGGCGGCGAGTTGCACGGTG 1212
Db 1081 ACAAAGCTCGCTGAGAGCTCAAAATACAGACCTCTTGGAGCAGCAACTACAGGTG 1140
QY 1213 GGTGTGACGCTGGGGGCTGATATTCAAGCGGTTGTCGAAAAAGGAGTATGTGAAG 1272
Db 1141 GTTGGGCTGGGTGGGACTAATATTACGGCTCTCTCTCGTCAAGAAAAAGTACTTTGAAC 1200
QY 1273 AGTTTACGGGTTG-----GGGAGGCGCACGGGTTGCTCATGGGGGTGGTGGAACT 1326
Db 1201 AGATTTACGGCAACAAACCCGGAAGGCACACGGTTGTTTATGGCGGTGGAGGAAAC 1260
QY 1327 TGCTGGGCGGCGACGTTGATTCAGATTCTGCTGATGCTGCTGGTGGTTCAGTGGCACTGG 1386
Db 1261 TACTTGAGCTCAGCTGATTCAGATCATTCAGCTTGGGTGGGTAACTGGGACCATGG 1320
QY 1387 GACCTTGTGTTGGGGTTGAATAAAGTGAAGCTGTTGAGGATTTCTTCAGAGGATGAGC 1446
Db 1321 GGACACTTTTCTCATCTCAAGAAATGAATGTTGCGGATATCGTCCGAGATGAGA 1380
QY 1447 TTGGGGGATGGACATGACTCGCCATGGAGCTTTCGTTATGCTTATGAGGATGATGAGA 1506
Db 1381 TGGCGGTATGATATGACCGACCGGCTGTTTCTTATATGTTACTTTGATGATG 1440
QY 1507 CGCACAGCATGGATCGAGTTGAGGAGGTTGGGCGCAACGGTCTTCACACCCACCA 1566
Db 1441 AGTCTCAAGACCATTCAGTTAGGAGATTGAGCAAGATCTCTCTCTCTCTCTCTCT 1500
QY 1567 CTGAT 1571
Db 1501 CTAAT 1505

RESULT 2

US-09-249-585A-4

; Sequence 4, Application US/09249585A

; Patent No. 6417002

; GENERAL INFORMATION:

; APPLICANT: Horlick, Robert

; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES

; FILE REFERENCE: 0867/0905

; CURRENT APPLICATION NUMBER: US/09/249,585A

; CURRENT FILING DATE: 1999-02-11

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4

; LENGTH: 1926

; TYPE: DNA

; ORGANISM: Epstein Barr Virus

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1) - (1926)

; OTHER INFORMATION: template strand of EBNA-1 DNA

US-09-249-585A-4

Query Match

Best Local Similarity 5.4%; Score 91.4; DB 4; Length 1926;

Matches 290; Conservative 0; Mismatches 331; Indels 0; Gaps 0;

QY 110 CCAACTTCTCGCGCCCAACACACAGAGCGCTCGCGCGCGCTCCCTTATCTGCGGCCA 169
Db 259 CCACTTCT 318
QY 170 TTTCGCGCGCTGGACAGCAAGTTTCGTCGACAGCGGCTTCGCGCTGCAACACCTACCT 229

	QY	230	CCTCTTTTCCGCGCTACCTCGTTTTTTCTATGCAGCTCGGGTTCGCCAATGCTCTGCGCCGG	289
	Dd	379	CCTCCTCCCCTCTCTCGTCTCTCCCGCTCTCCCGCTCTCCCGGTCTCTCGTCTCTCT	438
	QY	290	CTCCGCTCGCGCCGAAGAACAACATGAACATCATGCTCACCAACGTCTTGAGACTGCCCGC	349
	Dd	439	CCCCGTCTCGTCTCCTCTCCCGTCTCCCGTCTCTCTCTCCCGGTCTCTCCCGT	498
	QY	350	GGCGGGCTCTTCTATCACTTCTTGGGCTTGCGCTTTTGGCTTCGCCCTCCAAACGG	409
	Dd	499	CCTCCCGTCTCTCGTCTCTCTCCCGCTCTCGTCTCTCCCGGTCTCTCCCGTCTCTCGT	558
	QY	410	CTTTCATCGGTAAAATTCTTTCGGCCTCAAGGACATCCCTTCATCTCTCTACGACTACAG	469
	Dd	559	CTCTCTCCCGGTCTCTCCCGTCTCTCCCGTCTCTCGTCTCTCCCGGTCTCTCGTCTCTCC	618
	QY	470	CTACTTCTCTATACMAATGGGGCTTCGGCATCGCGCGCGCGGATACACAGCGAAGCAT	529
	Dd	619	CGTCTCTCCCGTCTCTCCCGTCTCTCGTCTCTCCCGGTCTCTCGTCTCTCTCCCGTCTCTCC	678
	QY	530	CGCCGAAAGCACACAGATTGCGGGCTATCTCATCTACTCTCTCTCTCTCACCGGCTTCGT	589
	Dd	679	CGTCTCTCCCGTCTCTCGTCTCTCCCGTCTCTCGTCTCTCCCGGTCTCTCGTCTCTCCCGTCTCT	738
	QY	590	CTATCCGGTGTCTCCCACTGGTTCTGGTCCCAAGCGGTGGGCTCTGCTTTTAAGAT	649
	Dd	739	CGTCTCTCCCGTCTCTCCCGTCTCTCGTCTCTCCCGGTCTCTCCCGGTCTCTCGTCTCTCCCGT	798
	QY	650	CACCGAACGGGTATTTTCCACGGCGATAAGACTTCGCGCGGTTCCGGGGCTAGTCCACAT	709
	Dd	799	CTCTCCCGTCTCTCGTCTCTCTCCCGTCTCTCCCGTCTCTCGTCTCTCTCCCGTCTCTCC	858
	QY	710	GGTCGGCGGAATAGCGGCT	730
	Dd	859	CGTCTCTCTCTCCCGTCTCT	879

RESULT 4
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:

Sequence 14, Application US/0823246.
Patent No. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
Zip: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZ9pt-Fls
IS-08-232-463-14

Query Match 4.8%; Score 82; DB 1; Length 7218;
Best Local Similarity 6.7%; Pred. No. 5e-10;
Matches 28; Conservative 241; Mismatches 151; Indels 0; Gaps 0;
175 CGCCGCGACAGCAAGTTCGTCGACACGCGCTTCGCGTCGACACACCTACCTCTCT 234
1033 CGAGCTTGGCTCGAGTCGAGGAGCTTGCATTTTTTTTTTTTTTTTTTTTTT 1092
235 TTTCCGCTACCTCGTTTTTTTATGACGCTCGGCTTCGCCATGCTTCGCCGCGCTCCG 294
1093 YY 1152
295 TCGCGCGAAGAACATGACATCTCTCACCAGCTCTGACGCTCGCGCGCG 354
1153 YY 1212
355 GCCTCTTCTACTACCTTCGCGCTTCGCTTCGCTTCGCTTCGCCCTCCACGCTCA 414
1213 YY 1272
415 TCGGTAAACATTTCTTCGCGCTCAAGGACATCCCTCTCCTCTACGCTACGCTACT 474
1273 YY 1332
475 TCCTCTACCAATGGGCTTCGCCATCGCGCGCGCGGATCACCAGCGAAGCATCGCG 534
1333 YY 1392
535 AAGCAGCAGTTCGCGCTATCTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTATC 594
1393 YYGTACCAATCTCTATC 1452
RESULT 5
US-09-197-649-7/c
; Sequence 7, Application US/09197649
; Patent No. 6194550
; GENERAL INFORMATION:
; APPLICANT: Tuerk, Craig
; APPLICANT: Pribnow, David
; APPLICANT: Smith, Jonathan D.
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
; FILE REFERENCE: NEX02/C1-CON
; CURRENT APPLICATION NUMBER: US/09/197,649
; CURRENT FILING DATE: 1998-11-23
; EARLIER FILING DATE: 07/829,461
; EARLIER FILING DATE: 1992-01-31
; EARLIER APPLICATION NUMBER: 07/739,055
; EARLIER FILING DATE: 1991-08-01
; EARLIER APPLICATION NUMBER: 07/561,968
; EARLIER FILING DATE: 1990-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence

; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
; OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7

Query Match 4.5%; Score 76.6; DB 3; Length 390;
Best Local Similarity 50.1%; Pred. No. 2.7e-09;
Matches 190; Conservative 0; Mismatches 189; Indels 0; Gaps 0;
163 GCGGCATTTTCGCGCGCTGACAGCAAGTTCTGTCGACACGCGCTTCGCGTCGACAA 222
379 GCAACATGGCGT 320
223 CTTACTCTCTTTTCGCGCTACCTGTTTTCATGACGCTCGGCTTCGCGCTCTCTCT 282
319 TGTGCTGT 260
283 GCGCGGCTTCGTCGCGCGCAAGAACACCATGATCAATCATGCTCACCAGCTCTCGACG 342
259 TGTGCTGT 200
343 CTGCGCGCGCGCT 402
199 TGTGCTGT 140
403 CCAACGGCTTCATCGGTAACATTTCTTCGCGCTCAAGGACATCCCTTCATCTCTTACG 462
139 TGTGCTGT 80
463 ACTACAGCTACT 522
79 TGTGCTGT 20
523 GAAGCATCGCGAAGGAC 541
19 TGTGCTGT 20
RESULT 6
US-09-249-585A-2/c
; Sequence 2, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein Barr Virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1926)
; OTHER INFORMATION: coding strand of EBNA-1 DNA
US-09-249-585A-2
Query Match 4.5%; Score 76; DB 4; Length 1926;
Best Local Similarity 47.2%; Pred. No. 7.8e-09;
Matches 232; Conservative 0; Mismatches 260; Indels 0; Gaps 0;
137 CGCTCCGCGCGCGCT 196
745 CTCCTGCT 686
197 CGACACGGCTTCGCGCTCGACACACCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 256
685 CTCCTGCCCT 626
257 TATGACGCTCGGCTTCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 316

317 CATCATGCTCACAAAGCTCTGAGAGCTGCGCGCGGCGCTCTTCTACTACTCTTCGG 376
1b 948 CTCCTCTGCTCTCTGCGCTCTCTGCGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTG 889
377 CTTGCGCTTCTGCTTCTGCGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTG 436
1b 888 CCGCTCTCTGCTCTCTGCGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTCTGCTCTG 829
437 CAAGGACATCT 496
1b 828 CTGCGCT 769
377 CATGCGCGCGCGCGCT 556
1b 768 CT 709
557 TCTCATCTACT 616
1b 708 CCGCT 649
617 GTCCCGACAGCG 628
648 TTCCACCGTGG 637

RESULT 9

S-09-359-081-2/c

Sequence 2, Application US/09359081

Patent No. 6316223

GENERAL INFORMATION:

APPLICANT: Liao, Ying

Hiang, Betty

Pavan, Don

TITLE OF INVENTION: Mammalian Protein Interaction Cloning

NUMBER OF SEQUENCES: 5

CORRESPONDENCE ADDRESS:

ADDRESS: Flehr, Hobbach, Test, Albritton & Herbert

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-4187

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/359,081

FILING DATE: 22-Jul-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/050,863

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Silva, Robin M.

REGISTRATION NUMBER: 38,304

REFERENCE/DOCKET NUMBER: A-65638/DJB/RMS

TELEPHONE: (415) 949-8711

TELEFAX: (415) 949-8711

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2580 base pairs

TYPE: nucleic acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 2:

S-09-359-081-2

Query Match 4.5%; Score 76; DB 4; Length 2580;
Best Local Similarity 47.2%; Pred. No. 8.9e-09;
Matches 232; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

QY 137 CGCGTCGCGCGCGCT 196
DB 1128 CTCCTGCT 1069
QY 197 CGACACGCGCT 256
DB 1068 CTCCTGCGCT 1009
QY 257 TATGAGCT 316
DB 1008 CTCCTGCGCT 949
QY 317 CATCATGCTCACAAAGCT 376
DB 948 CTCCTGCT 889
QY 377 CTTGCGCTTCTGCTTCTGCGCT 436
DB 888 CCGCTCTCTGCT 829
QY 437 CAAGGACATCT 496
DB 828 CTGCGCT 769
QY 497 CATGCGCGCGCGCGCT 556
DB 768 CTCCT 709
QY 557 TCTCATCTACT 616
DB 708 CCGCT 649
QY 617 GTCCCGACAGCG 628
DB 648 TTCCACCGTGG 637

RESULT 10

US-09-130-114-1

Sequence 1, Application US/09130114

Patent No. 5976807

GENERAL INFORMATION:

APPLICANT: Horlick, Robert A.

APPLICANT: Damaj, Bassam B.

APPLICANT: Robbins, Alan K.

TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes

TITLE OF INVENTION: From Multiple Transfected Episomes

FILE REFERENCE: 0867/1D903US1

CURRENT APPLICATION NUMBER: US/09/130,114

CURRENT FILING DATE: 1998-08-06

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 1

LENGTH: 5452

TYPE: DNA

ORGANISM: VEBNA

US-09-130-114-1

Query Match 4.5%; Score 76; DB 2; Length 5452;
Best Local Similarity 47.2%; Pred. No. 1.2e-08;
Matches 232; Conservative 0; Mismatches 260; Indels 0; Gaps 0;

QY 137 CGCGTCGCGCGCGCT 196
DB 1677 CTCCTGCT 1736
QY 197 CGACACGCGCT 256
DB 1737 CTCCTGCGCT 1796

121 GCCAAACACACAGACGCGCTCCGCGCGCGCTCCCTTATCTGCGGCCATTTTCGCGCGC 180
181 TGACAGCAAGTTCTGTCGACAGCGCTTCGCGCTCGACAAACACCTACCTCTCTTTTCG 240
181 TGACAGCAAGTTCTGTCGACAGCGCTTCGCGCTCGACAAACACCTACCTCTCTTTTCG 240
241 CTTACTCTGTTTCTATGCAAGCTGGCTTCGCCATGCTCTGCGCCGCGCTTCGCGCG 300
241 CTTACTCTGTTTCTATGCAAGCTGGCTTCGCCATGCTCTGCGCCGCGCTTCGCGCG 300
301 CCAAGAACCACTGACATGCTCAACAAAGCTCTGACGCTCGCGCGCGCGCTCT 360
301 CCAAGAACCACTGACATGCTCAACAAAGCTCTGACGCTCGCGCGCGCGCTCT 360
361 TCTACTACCTCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 420
361 TCTACTACCTCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 420
421 AACATTTCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCG 480
421 AACATTTCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCG 480
481 ACCAATGGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 540
481 ACCAATGGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 540
541 CACAGTTCTGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 600
541 CACAGTTCTGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 600
601 TCTCCCACTGGTTCTGCTCCCGACAGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 660
601 TCTCCCACTGGTTCTGCTCCCGACAGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 660
661 TATTTTCCACCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 720
661 TATTTTCCACCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 720
721 TAGCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 780
721 TAGCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 780
781 GACGAGCTGGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 840
781 GACGAGCTGGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 840
841 TTTGGTTCTGCTGCTACGATTTAACCCTGCTTCATTTAAACAAATCTCTACTTCTACG 900
841 TTTGGTTCTGCTGCTACGATTTAACCCTGCTTCATTTAAACAAATCTCTACTTCTACG 900
901 GTAACTCAGAAATTTACTAGCTCAATGAGCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 960
901 GTAACTCAGAAATTTACTAGCTCAATGAGCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 960
961 CCTAGCGGGTCAACAGCTGCTTACCGCTCAATGAGCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 1020
961 CCTAGCGGGTCAACAGCTGCTTACCGCTCAATGAGCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 1020
1021 ACTGGAACGTGACCGGCTGCTGCAACCGGCTGTTAGCGGCTTCGCGCTTCGCGCTTCGCGCTTCG 1080
1021 ACTGGAACGTGACCGGCTGCTGCAACCGGCTGTTAGCGGCTTCGCGCTTCGCGCTTCGCGCTTCG 1080
1081 GTTGTCTCGGTGTTGACCTAGCGGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 1140
1081 GTTGTCTCGGTGTTGACCTAGCGGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCGCGCTTCG 1140
1141 TAATAGCTTGCAACAAATAGCAGAGAGGTTAAGTTGCAAGATCTCTGAGCGCGCGC 1200
1141 TAATAGCTTGCAACAAATAGCAGAGAGGTTAAGTTGCAAGATCTCTGAGCGCGCGC 1200
1201 AGTTGACGCTGGGTGTCGACGTTGGGGGTGATTTTCAACGCGGTTGTTCCAAAAAGG 1260
1201 AGTTGACGCTGGGTGTCGACGTTGGGGGTGATTTTCAACGCGGTTGTTCCAAAAAGG 1260

QY 1261 AGTATGTGAGGAGTTTACCGGTTGGGAGCGCGACGGGTTGCTCATCGGSGTG 1320
DB 1261 AGTATGTGAGGAGTTTACCGGTTGGGAGCGCGACGGGTTGCTCATCGGSGTG 1320
QY 1321 GGAATTTCTGCGCGCGCACTGATTGAGTTTGGTGAATTTGCTGGGTTAGTCCGA 1380
DB 1321 GGAATTTCTGCGCGCGCACTGATTGAGTTTGGTGAATTTGCTGGGTTAGTCCGA 1380
QY 1381 CCATGGGACCTTCTTTGGGGTTGAATAAAGCTGTTGAGGATTTCTTCAGAGG 1440
DB 1381 CCATGGGACCTTCTTTGGGGTTGAATAAAGCTGTTGAGGATTTCTTCAGAGG 1440
QY 1441 ATGAGCTTCGCGGGATGACATGCTGCCATGAGGCTTTGCTTATGCTTATGAGGATG 1500
DB 1441 ATGAGCTTCGCGGGATGACATGCTGCCATGAGGCTTTGCTTATGCTTATGAGGATG 1500
QY 1501 ATGAGCGCAACGAGCTGGGATGAGTTGAGGAGGTTGGGCGCAACGGCTTCACAC 1560
DB 1501 ATGAGCGCAACGAGCTGGGATGAGTTGAGGAGGTTGGGCGCAACGGCTTCACAC 1560
QY 1561 CCACCACTGATGATGATCTTTTTCCTATATGCTGCTCATTAAGTCAAAAT 1620
DB 1561 CCACCACTGATGATGATCTTTTTCCTATATGCTGCTCATTAAGTCAAAAT 1620
QY 1621 TTGGATACATATTCCTGTAAGGATTCAGGCTTCAGGCTTCGTTACTTCTGTTAAAAA 1680
DB 1621 TTGGATACATATTCCTGTAAGGATTCAGGCTTCAGGCTTCGTTACTTCTGTTAAAAA 1680
QY 1681 AAAAAA 1706
DB 1681 AAAAAA 1706

RESULT 2

US-10-424-599-139317
; Sequence 139317, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 139317
; LENGTH: 2162
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_96810C.1
US-10-424-599-139317

Query Match 97.7%; Score 1666.2; DB 12; Length 2162;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 CGAGCACTCCCAACCCCAACCCGAGTTTCTACCACTTCAGTCAGCGGTATACACTA 63
DB 47 CCACCACTCCCAACCCCAACCCGAGTTTCTACCACTTCAGTCAGCGGTATACACTA 106
QY 64 ACCAACCCCAACCTTCGCTGCTTCGCGCGCAACCTTCGCGCGCACTTCTCGGCC 123
DB 107 ACCAACCCCAACCTTCGCTGCTTCGCGCGCAACCTTCGCGCGCACTTCTCGGCC 166
QY 124 CAAACACCAAGAGCCCTCCGCGCGCTTCCTTATCTGCGGCACTTCGCGCGCTGG 183
DB 167 CAAACACCAAGAGCCCTCCGCGCGCTTCCTTATCTGCGGCACTTCGCGCGCTGG 226

184 ACAGCAAGTTCTGTCGACACGGCTTTCGGCGTCGACAAACCTCTCTCTTTTCGGCT 243
185
227 ACAGCAAGTTCTGTCGACACGGCTTTCGGCGTCGACAAACCTCTCTCTTTTCGGCT 286
228
244 ACCTCGTTTTTTCTATGACAGCTCGGCTTCGGCATCTCTGCGCGGGTTCGGTCGGCGCA 303
245
287 ACCTCGTTTTTTCTATGACAGCTCGGCTTCGGCATCTCTGCGCGGGTTCGGTCGGCGCA 346
288
304 AGAACACCATGAAATCATGCTCAACAGCTCTGGAAGCTTCGGCGCGGGCTCTCTCT 363
305
347 AGAACACCATGAAATCATGCTCAACAGCTCTGGAAGCTTCGGCGCGGGCTCTCTCT 406
348
364 ACTACCTCTTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 423
365
407 ACTACCTCTTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 466
408
424 ATTCTTCGGCTTCAGGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 483
425
467 ATTCTTCGGCTTCAGGACATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 526
468
484 AATGGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 543
485
527 AATGGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 586
528
544 AGTTCGTGGCTTCATCT 603
545
587 AGTTCGTGGCTTCATCT 646
588
604 CCACCTGGTTCTGTCGTCGACAGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 663
605
647 CCACCTGGTTCTGTCGTCGACAGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 706
648
664 TTTCCACCGGCTTAATAGACTTCGCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 723
665
707 TTTCCACCGGCTTAATAGACTTCGCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 766
708
724 CGGCTATGGGAGCGCTATGATGAGGCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 783
725
767 CGGCTATGGGAGCGCTATGATGAGGCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 826
768
784 GAGCTGTGGCTTCGAGGCGCACAGCGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 843
785
827 GAGCTGTGGCTTCGAGGCGCACAGCGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 886
828
844 GGTTCGTGGTTCAGGATTAACCGGCTTCATTTAACAATCTCTACTTACTTACGGTA 903
845
887 GGTTCGTGGTTCAGGATTAACCGGCTTCATTTAACAATCTCTACTTACTTACGGTA 946
888
904 ACTCAGGAATTAATACGCTCAATGAGCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 963
905
947 ACTCAGGAATTAATACGCTCAATGAGCGGCTTCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 1006
948
964 TAGCGGGTCAACAGCTGCTTCGACCGCTATTCGGTAAACCGGCTGATTCGGGTCACT 1023
965
1007 TAGCGGGTCAACAGCTGCTTCGACCGCTATTCGGTAAACCGGCTGATTCGGGTCACT 1066
1008
1024 GGAAGCTGACCGATCTGCAACCGGCTTCGAGCGGCTTCGGCTTCGGCTTCGGCTTCGGCT 1083
1025
1067 GGAAGCTGACCGATCTGCAACCGGCTTCGAGCGGCTTCGAGCGGCTTCGGCTTCGGCTTCGGCT 1126
1068
1084 GCTCGGTGGTTCGAGCATGGGCGGCTTCGATGCGGCTTCGATGCGGCTTCGATGCGGCTTCGAT 1143
1085
1127 GCTCGGTGGTTCGAGCATGGGCGGCTTCGATGCGGCTTCGATGCGGCTTCGATGCGGCTTCGAT 1186
1128
1144 TAGCTTCGAACAAATAGCAGAGGTTAGTTCGAGGCTTCGAGCGGCTTCGAGCGGCTTCGAG 1203
1145
1187 TAGCTTCGAACAAATAGCAGAGGTTAGTTCGAGGCTTCGAGCGGCTTCGAGCGGCTTCGAG 1246
1188
1204 TGCAGCTGGGTTCGACAGCTGGGCGGCTTCGATGCGGCTTCGATGCGGCTTCGATGCGGCTTCGAT 1263
1205
1247 TGCAGCTGGGTTCGACAGCTGGGCGGCTTCGATGCGGCTTCGATGCGGCTTCGATGCGGCTTCGAT 1306
1248
1264 ATGTGAAGAGGTTTACGGGTTGGGAGGGCGGCTTCGATGCGGCTTCGATGCGGCTTCGATGCGGCTTCGAT 1323

1307 ATGTGAAGAGGTTTACGGGTTGGGAGGGCGCACCGGTTGCTCATGGGGGTGGTGGGA 1366
1308
1324 AGTTCTCGCGCGCACGCTGATTCAGATTCCTGGTGAATTCCTGGTGGGTAGTTCGACCA 1383
1325
1367 AGTTCTCGCGCGCACGCTGATTCAGATTCCTGGTGAATTCCTGGTGGGTAGTTCGACCA 1426
1368
1384 TGGGACCTTTCTTTTGGGGTTGAATAAATCTGAAGCTGTTGAGGATTTCTTCAGAGGATG 1443
1385
1427 TGGGACCTTTCTTTTGGGGTTGAATAAATCTGAAGCTGTTGAGGATTTCTTCAGAGGATG 1486
1428
1444 AGCTTCGCGGATGAGCATGCTGCGCATGAGGCTTTGCTTATGCTTATGAGGATGATG 1503
1445
1487 AGCTTCGCGGATGAGCATGCTGCGCATGAGGCTTTGCTTATGCTTATGAGGATGATG 1546
1488
1504 AGAGCACAAGCATGGGATGAGTTGAGGAGGTTGGGCCCAACGGGCTTCCTCCACCCCA 1563
1505
1547 AGAGCACAAGCATGGGATGAGTTGAGGAGGTTGGGCCCAACGGGCTTCCTCCACCCCA 1606
1548
1564 CCACCTGATGATGATCTTTTCCCATATGCTATGCTCTCATTTAGTCAACATTAATTTG 1623
1565
1607 CCACCTGATGATGATCTTTTCCCATATGCTATGCTCTCATTTAGTCAACATTAATTTG 1666
1608
1624 GATACATATTCCTTTGAAGGATTCAAACCTTGGTTACTTCTTCTGTTAAAAAAA 1692
1625
1667 GATACATATTCCTTTGAAGGATTCAAACCTTGGTTACTTCTTCTGTTAGATCAA 1725
1668

RESULT 3

US-10-033-109-5
; Sequence 5, Application US/10033109
; Publication No. US20020142390A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/10/033,109
; CURRENT FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: 09/384,625
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 5
; LENGTH: 1991
; TYPE: DNA
; ORGANISM: Triticum aestivum
US-10-033-109-5

Query Match 45.1%; Score 768.6; DB 13; Length 1991;
Best Local Similarity 73.8%; Pred. No. 2.2e-193;
Matches 991; Conservative 0; Mismatches 349; Indels 3; Gaps 1;
QY 174 CCCCGCGTGGACAGCAAGTTTCGTCGACACGGCTTCGCGTCGACAGCAACCTACCTCTCC 233
DB 134 GACTACCTGTGCAACAGGTTTCGCGGACACACACGTCGCGGTGGACTCCACCTACCTGCTC 193
QY 234 TTTTCCCGCTACCTCTCGTTTTTTTCTATGACGCTCGGCTTCGCCATGCTCTGCGCGGCTCC 293
DB 194 TTTTCGGCTACCTCTCGTTTTTCGCCATGCGAGTCGGCTTCGCCATGCTCTGCGCGGCTCC 253
QY 294 GTCCGCGCCGAAGAACACCATCATCTCACCAGTCTCTGAGACGCTGCGCGCGGCG 353
DB 254 GTCCGCGCCGAAGAACACCATCATCTCACCAGTCTCTGAGACGCTGCGCGCGGCGGCG 313
QY 354 GGCCTCTTCTACTACCTCTTCGGCTTCGCGCTTCGCTTTCGGCTTCGCCCTCCAAACGGCTTC 413
DB 314 GCGCTCTTCTACTACCTCTTCGGCTTCGCGCTTCGCTTTCGGGAGCGGCTCGAAGCGCTTC 373
QY 414 ATCGGTAAACATTTCTTCGGGCTCAAGGACATCCCTTCATCTCTACGACTACAGCTAC 473

733 GGGGAGCGCTGATCGAAGGCCCAAGAAATGGAGCGTTTCGATCATGACGAGCAGCGTGTGG 792
Db |||||
644 GGGGTGGCTCATCGAAGGTCACAGACTTGGCGGTTCGATAACGAGGCGCGTGCATCG 703
Qy CTTTGGAGGCCACAGCGCGTCTTGTAGTAGTCTCGGAAACCTTCTTGTCTTGTGTTGGTT 852
Db CTTCTGTGGCCACTCGGCGCTCACTTGTGTCTTGTGACATCTCTCTCTGTGTTGGAT 763
2y GGTACGATTTAACCCCGGTTCAATTAACAAATCCTACTTACTTACGTTAACTCAGAA 912
Db GGTACGATTTAACCCCGGTTCTTCAACAAATCCTACTTACTTACGTTAACTCAGAA 820
913 ATTACTACGCTCAATGAGGCGGCTTGGCAGAACCGCGTCCACTACCTAGCGGGT 972
Db CATACACGCGGCTGAGCGGCTCGGAGGACAGCTGTCAACACAGTTAGTGTGCT 880
973 CAACAGTCTGCTGACACGCTATTCGTTAAACGGGTGATATCCGGTCACTGGAACGTGA 1032
Db GCACCGCGGCGCTGACAAACCTTATTTGGGAAACGCTCTACTCTCGGGAATTTGGAACGTCA 940
1033 CCGATGCTCTCAACCGGCTCTTAGGCGGTTTCGCGCGGATACACGCGGTTGCTCCGTGG 1092
Db CTGATGATGACACGCGCTCTCGAGGTTTTCGAGCCATTAATCTGTGCTCTGTGCTG 1000
1093 TTGAGCCATGGGCGAGCACTGATGAGCGTTTGTGCTTCTATAGTATTAATAGCTTGA 1152
Db TTGAGCCATGGGCGTGGATCATCTGCGGTTTGTGCGGCGCTTCTCTCTCTCTCTCTCT 1060
1153 ACAATTAGCAGAGAGGTTAAGTTCGAGGATCTTGGAGCGGCGGCGGCTTCTCTCTCTCT 1212
Db ACAAGTCTGCTGAGAGCTCAATACGACGCTTCTGAGCGGCTTCTCTCTCTCTCTCTCT 1120
1213 GGTGCGCAGTGGGCGGTGATATTCACGCGGTTTTCGCAAAAGAGGATGTGAAGG 1272
Db GTTGGCGTGGTGGGACTAATATTCAGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1180
1273 AGGTTTACGCGTTG-----GGAGGCGCAGCGGTGCTCATGGGCGGTGGTGAAGT 1326
Db AGATTTACGCAACAAACCGGAGGCGCACGCGTTGTTATGCGCGGTGGAGGAAAC 1240
1327 TGTGCGGCGCAGCTGATTCAGATTCGCTGATTCGCTGGGTGAGTTCGACCACTGG 1386
Db TACTTGGAGCTCAGCTGATTCAGATTCATGTCATCAGCGGTTGGTGAAGTGGACCATGG 1300
1387 GACCTTGTGTTGGGCGTTGAATAACGACGCTTGGAGATTTCTTCAGAGTACGAC 1446
Db GGACATTTTCTTCATCTCAAGAAATGAAATGTTGCGGATATCGTCCGAGGATGGA 1360
1447 TTGCGGCGATGACATGACTCGCCATGAGGCTTTCGCTTATGCTTATGAGGATGATGGA 1506
Db TGCGCGGTATGATATGACGAGCGGCTGTTTGTCTTATATGATGATGATGATG 1420
1507 CGCACAGCATGGATGAGTTCAGTTCAGAGGCGGTTGGGCGCAACGCGTCTTCCACACCA 1566
Db AGTCTCACAAGCCATTCAGCTTAGAGAGTTGAGCCAGATCTCTCTCTCTCTCTCTCTCT 1480
1567 CTGAT 1571
Db CTAAT 1485

RESULT 5
US-09-938-842A-1203
Sequence 1203, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REFERENCE: SCRIPT1300-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1203
LENGTH: 1506
TYPE: DNA
ORGANISM: Arabidopsis thaliana
US-09-938-842A-1203

Query Match 44.3%; Score 755.8; DB 11; Length 1506;
Best Local Similarity 71.7%; Pred. No. 4.8e-190;
Matches 1036; Conservative 0; Mismatches 397; Indels 12; Gaps 3;

Qy 136 AGCCTCCGCGCGCGCTTCTTATCTGGGCGCATTCGCGCGGTGGACAGCAAGTTCG 195
Db 44 ATGCCACGCGCGCGCGCAACTACATCTGTGCCAGTTAGGCGAGCTCAACACAAATTTA 103
Qy 196 TCGACACGCGCTTCGCGCTCGACACACCTTACCTCTCTTTCGCGCTACCTCTCTTTT 255
Db 104 TCGACACGCGCTTCGCTATAGACACACTTACCTCTCTTTCGCGCTACCTCTCTTCT 163
Qy 256 CTATGAGCTCGGCTTCGCGCTGCTCTGCGCGGCTGCTCGCGCGCAAGAACCACTGA 315
Db 164 CTATGAGCTTCGCTTCGCTATGCTCTGTGCGGTTCCGTGAGAGCCAAAGTAATATGA 223
Qy 316 ACATCATGCTCACCAACGCTCTGAGCGCTGCGCGCGGCTCTTCTACTACTCTCTTCG 375
Db 224 ACATCATGCTTACCAACGCTCTGAGCGTGCAGCGGTGCTCTCTCTCTCTCTCTCT 283
Qy 376 GCTTGGCTTCGCTTCGCGCTCCGCTCCGCTTCAAGCGCTTCATCGGTAACATTTCTTGG 435
Db 284 GCTAGCGCTTTCGCTTCGCTTCAATGCTTTCGCTTCAATGCTTTCGCTTAAACACT 343
Qy 436 TCAAGGACATCCCTTCATCTCTTACGCTACAGCTACTTCTCTCTCTCTCTCTCTCT 495
Db 344 TCAAGACATCCCCACGCGCTCTGCTGACTCTCAACTTCTCTCTCTCTCTCTCTCT 403
Qy 496 CCATCGCGCGCGCGCATCACAGCGGAGCATGCGCGCAACGACACAGTTCGTCGCGCT 555
Db 404 CAATCGCTCGCGCTGGAATCAAGTGCCTGCTGCTGAAACGACACAGTTCGTCGCT 463
Qy 556 ATCTCATCTACT 615
Db 464 ACCTAATCTATCT 523
Qy 616 GGTCCCCAGACGCTGGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 672
Db 524 GGTCAAGTTCAGTGGAGTGGCGCAGCGCTTCCGATCCGATGGAGATTTGCTTTTCAG 583
Qy 673 CGTAAATAGATTCGCGCGGTTCGCGCTAGTCCACATGCTCGCGGAAATAGCGCGCTAT 732
Db 584 GAGCGATAGATTCGCTGCGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 643
Qy 733 GGGGAGCGCTGATCGAAGGCCCAAGAAATGGAGCGTTTCGATCATGACGAGCAGCTGTGG 792
Db 644 GGGGTGGCTCATCGAAGTTCACAGCTTGGCGGTTTCGATACGAGGCGCGTGCATCG 703
Qy 793 CTTTGGAGGCCACAGCGGCTCTTGTAGTCTCTGGAAACCTTCTCTCTCTCTCTCTCT 852
Db 704 CTTTCTGTGGCCACTCGGCGCTCACTTGTGTCTCTTGGAAACATTCCTCTCTCTCT 763
Qy 853 GGTACGATTTAACCCCGGTTCAATTAACAAATCCTACTTACTTACGTTAACTCAGAA 912
Db 764 GGTACGATTTAACCCCGGTTCTTCAACAAATCCTACTTACTTACGTTAACTCAGAA 820
Qy 913 ATTACTACGCTCAATGAGGCGGCTTGGCAGAACCGCGGTCACCACTACCTAGCGGGT 972

821 CATACACGCCAGTGGAGCGGTCGGACGACGCTGTCAACACAGCTTACCTGGCT 880
973 CAACAGCTCCTTGACCAAGCTATTTCGGTAAACGGGTGATTCGGTCACTTGGAACTGA 1032
881 GCACCGCGCGCTGACCAACCCCTATTTCGGGAAACGCTACTCTCGGGACATTGGAACTCA 940
1033 CGATCTCTGCAACCGGCTGTAGCGGTTTCGGCGGATTAACAGCCGGTGTCTCCGGTG 1092
941 CTGATGTATGCAACGCCCTCCTCGAGGGTTGACAGCCATACTAAGTGGTGTCTCTCG 1000
1093 TTGAGCCATGGGAGCAGCATGATGCGGTTTGTGCTTCTATAGTATTAATAGCTTGA 1152
1001 TTGAGCCATGGGCTGATGATCTCGCGGTTTCGGCGGCTTGTCTCTCGATGCA 1060
1153 ACAAAATTACAGAGAGGTAAAGTTTCGACGATCTCTGAGCGCGCGAGTTGCACGGTG 1212
1061 ACAAGCTCCTGAGAAGCTCAATACGACGCCCTCTTGAGGACGACAACTACAGGTTG 1120
1213 GGTGTGGCAGCTGGGGGGTGATTAATTCAGCGGTTGTTTCGCAAAAAGAGTATGTGAAG 1272
1121 GTTGGCGGTGCTGGGAGCTAAATTACAGGCTCTCTCGCTCAAGAAAAGTACTTGAAC 1180
1273 AGGTTTACCGGTTG-----GGAGCGGCGACGGGTTGCTCATGGGGGTGGTGGAGT 1326
1181 AGATTTCAGGCAACAAACCCGGAAGCCACACGGTTGTTTATGGCGGTGGAGAAAC 1240
1327 TGTGCGCGGCGACGTGATTCAGATCTGTTGATGTTGCGGTGAGTGGCGACCATGG 1386
1241 TACTTGGAGCTCAGCTGATTCAGATCAATGTTGATCACGGTTGGGTAAGTGGACCATGG 1300
1387 GACCTTGTGTTGGGGTGTGAATAAATGAACTGTTGAGGATTTCTTCAGAGATGAGC 1446
1301 GGACACTTTTCTTCTCCTCAGAAAATGAAATGTTGCGGATATCGTCCGAGATGAGA 1360
1447 TTGCGGGATGACATGATCTGCCATGAGGCTTGTCTTATGCTTATGAGGATGATGAGA 1506
1361 TGCGCGGTATGATATGACAGGCGCGTGGTTTGTCTTATATGATCTTATGATGATG 1420
1507 CGCACAGCATGCGATGAGTTGAGGAGGTTGGCCCAACGCTCTTCCACACCCACCA 1566
1421 AGTCTCAAAAGCATTCAGCTTAGAGAGTTGAGCAAGATCTCTCTCTCTCTCTCT 1480
1567 CTGAT 1571
1481 CTAAT 1485

RESULT 6

US-08-635-967-1
Sequence 1, Application US/08635967
Publication No. US20010003848A1
GENERAL INFORMATION:
APPLICANT: FROMMER, Wolf-Bernd
APPLICANT: NINNEAN, Olaf
TITLE OF INVENTION: DNA SEQUENCES FOR AMMONIUM TRANSPORTER,
TITLE OF INVENTION: PLASMIDS, BACTERIA, YEASTS, PLANT CELLS AND PLANTS
TITLE OF INVENTION: CONTAINING THE TRANSPORTER
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Ostrolenk, Faber, Gerb & Soffen, LLP
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10036-8403
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/635,967

FILING DATE: 29-APR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP 94/03499
FILING DATE: 24-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 43 37 597.9
FILING DATE: 28-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Meilman, Edward
REGISTRATION NUMBER: 24,735
REFERENCE/DOCKET NUMBER: P/951-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 382-0700
TELEFAX: (212) 382-0888
TELEX: 236925
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1748 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
INDIVIDUAL ISOLATE: Ammonium transporter
IMMEDIATE SOURCE:
LIBRARY: cDNA library in plasmid pF161
POSITION IN GENOME:
MAP POSITION: from 21 to 1523 coding region
FEATURE:
NAME/KEY: CDS
LOCATION: 21...1526
US-08-635-967-1
Query Match 44.3%; Score 755.8; DB 8; Length 1748;
Best Local Similarity 71.7%; Pred. No. 5.2e-190;
Matches 1036; Conservative 0; Mismatches 397; Indels 12; Gaps 3;
QY 136 ACGCTCGCGCGCGCTCCCTTATCTGCGGCATTTGCGCGCGTGGACAGCAAGTTGG 195
DB 64 ATGCCACGCGCGCGCACTACATATGTGCGCAGTAGCGGACGTCACACAAATTTCA 123
QY 196 TCGACACGCGCTTCGCGCTGACAAACACCTTACCTCTTTTCGCGCTACCTGTTTTT 255
DB 124 TCGACACGCTTCGCTATAGACAACTTACCTCTTCTCCGCTACCTGTCTTCT 183
QY 256 CTATGACGCTCGGCTTCGCCATGCTCTGCGCGGCTCGTCCGCGCAAGACACCATGA 315
DB 184 CTATGACGCTTCGCTATGCTCTGTCGCGGTTCGCGGAGCAAGAACTATGA 243
QY 316 ACATCATGCTCACCACAGCTCTGAGACGCTGCGCGCGGCGGCTTCTTCTACTACCTTT 375
DB 244 ACATCATGCTTACCAAGCTCTTGGAGCTGACGCGGTGCTCTTCTTATCTGTTG 303
QY 376 GCTTGGCTTCGCTTCGCGTCCCGCTCCGCGCTTCATCGGTAAACATTTCTTCGGCC 435
DB 304 GCTAGCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT 363
QY 436 TCAAGGACATCCCTTCATCTCTCTTACGACTACGACTTCTCTTCTTCTTCTTCTTCT 495
DB 364 TCAAGACATCCCGACGCGCTCTGCTGACTACTTCTTCTTCTTCTTCTTCTTCTTCT 423
QY 496 CCATCGCGCGCGCGGATCAGCAGCGGAGGATCGCGGAGCAACGACACAGTTTCTGTC 555
DB 424 CAATGCTGCGGCTGGAATCAAGTGGCTCGATGCTGAAACGACACAGTTCTGTCGCT 483
QY 556 ATCTCATCTACT 615
DB 484 ACCTAATCTATCT 543
QY 616 GGTCCCGACAGCGCTGGGCTCTGCTT---TAAATCACCGACCGGCTATTTTCCACCG 672

QY 903 AACTCAGGAATTAATCTACGGTCAATGAGCGCGTGTGGCAGAACCGCGTCACTACC 962
DB 1365 AGTGGAGGGTATATAT---GGTCAATGAGCGCTATAGGAGGACAGCTGTACAGCACA 1421
QY 963 CTAGCGGGGTCAACAGCTGCGTTGACACACCTATTTCGGTAAACGGGTGATATCCGGTAC 1022
DB 1422 TTGGCTGGAGACACTGCGGCTCTGACAGCGTTGTTTTCAGCAAGCGGTATTGGCTGCCAC 1481
QY 1023 TGGAACTGACCCGATGTCGCAACCGGCTGTAGGCGGTTTCGGCGCGATTAACAGCGGT 1082
DB 1482 TGGAACTGATGACGCTGTGACCGGCTGCTTGGCGGTTTCGCTGCCATTACTCGGCG 1541
QY 1083 TGCTCCGTGGTTGAGCCATGAGCAGCAGCATGATGATGCGGTTTGTGCTTCTATAGATTA 1142
DB 1542 TGTCCCGTGTGGAAACCGTGGCGCGGATTTGTGTGGGTTTGTGGCGCGGTGGGTTTG 1601
QY 1143 ATAGCTTGCAACAAATAGCAGAGAGGTTAAGTTCGACGATCCTCTGAGCGCGCGAG 1202
DB 1602 ATTGGGCTTAATAGCTTGCGCGAGGTAGATGATGATGATCCGTTGGAGCGCGCGAG 1661
QY 1203 TTGCACGGTGGTGTGCAAGTGGGGGGTGATATTCACGCGGTGTTTCGCAAAAAGGAG 1262
DB 1662 CTTTCACGCGCGGTGGAGCGGTGGGGGGTTTCTTTCACGCGGATTGTTTCGGAAGAAAGT 1721
QY 1263 TATGTGAAGAGGTTTACGGGTTGGGAGGCGCACGGGTTGCTCATGGGGGTGTGGG 1322
DB 1722 TACGTGAGGAGATTAAGCTTGTGAGGCGGTTTGTGAGGCGGTGGGAGG 1781
QY 1323 AAGTTGTGGCGGCGCATGATTCAGATTCGTGATTCGTGGGTTTGTGGGTTTGTGGG 1382
DB 1782 AGGCTGTGGCGGCGCATGATTCAGATTCGTGATTCGTGGGTTTGTGGGTTTGTGGG 1841
QY 1383 ATGGGACCTTGTGTTGGGGTGTGATAACTCAAGCTGTGAGGATTTCTCAGAGAT 1442
DB 1842 ATGGCGCGTGTGTTCTATGGGCTTCATAGATGAACTGTGAGAAATTCGAGGGATGAT 1901
QY 1443 GAGCTTGGGGGATGACATGACTCGCCATGAGGCTTGTCTTATGCTTATGAGGATGAT 1502
DB 1902 GAGACTGGGGATGGATTTGACAGGAGCATGGTGGGTTGCTTATGCAATACCATGATGAT 1961
QY 1503 GA 1504
DB 1962 GA 1963

RESULT 8

US-09-938-842A-1490
; Sequence 1490, Application US/09938842A
; Patent No. US2020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; PRIOR FILING DATE: 2001-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2000-08-24
; PRIOR FILING DATE: 2001-01-16
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1490
; LENGTH: 1545
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1490

Query Match

41.4%; Score 705.8; DB 9; Length 1545;

Best Local Similarity 70.3%; Pred. No. 9, 3e-177;
Matches 979; Conservative 0; Mismatches 402; Indels 12; Gaps 2;
QY 124 CAAACACACAGAGCGCTCCCGCGCGGCTCCCTTATCTCGGCGCATTTTCGCGCGGTGG 183
DB 62 CTAACTCAACATCTTCCCTCGCGCGGCAACCTTTTATGTTCCTTCAAAATTTCAACATCT 121
QY 184 ACAGCAAGTTCTGACAGCGGCTTCGCGCTGACACACCTACCTCTCTCTCTCTCGGCT 243
DB 122 CCAACAACTCTCCGACACAACTTATGCGCTGACACACAGTATCTCTCTCTCTCGGCT 181
QY 244 ACCTCGTTTTCTATGAGCTGCGCTTCGCAATGCTCTGCGCGGCTTCCTCTCGCGGCA 303
DB 182 ACCTTGTCTTTCGCAATGCGCTTCGCTTTCGCTATGCTTTCGCTGAGTACGTCGAGGCA 241
QY 304 AGAACACCATGAACATCATGCTCACCAAGCTTCGAGCGCTGCGCGCGCGGCGCTCTTCT 363
DB 242 AGAACACTATGACATCATGCTTACCAATGCTTCGCTGAGTTCGCGCTGGAGCATCTCTT 301
QY 364 ACTACCTTTCGCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 423
DB 302 ACTACCTTTCGCAATTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 361
QY 424 ATTTCTTCGCGCTCAAGGACATCCCTT-----CATCTCTCTACGACTACGACTACT 474
DB 362 ACATAGCTTCTTCGTTTACGCTCTTACCTGAGCGCGCGCTTCGACTTCAGCTTTT 421
QY 475 TCCTTACCAATGCGGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 534
DB 422 TCCTTACCAATGCGGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 481
QY 535 AACGCACACAGTTCTGCGCTTCATCTCATCTACTCTCTCTCTCTCTCTCTCTCTCTCTCT 594
DB 482 AGCAAGCAATTCGTTGCTTACCTTACTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCT 541
QY 595 CGGTGCTTCCCACTGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCG 651
DB 542 CGAGCTCTCGCACTGCTTCTGCTCAAGTATGATGGCTAGCGCGCTCCGCTCTGACA 601
QY 652 CCGACCGGCTATTTCCACCGGCTAATAGACTTCGCGGCTTCGCGGCTAGCTCCACATGG 711
DB 602 ACAATCTCTTGTGCTCAGGTGCTATGATTTTCAGGTTTCAGGAGTTGTTTCAATGG 661
QY 712 TCGCGGGAATAGCGCGCTTATGCGGAGCGCTGATCGAAGGCGCCCAAGAAATGGAGCTTTCG 771
DB 662 TAGTGGAAATTCGCGGTTTATGCGAGCGTTAGTTGAAGGACCAAGAAATAGTAGATTG 721
QY 772 ATCATGACGAGAGCTGTGGCTTCGAGGCGCACAGCGCTCTCTTAGTAGTCTCTGGAA 831
DB 722 ACCGTCAGCGCGGCTCCGCTTTCAGCTGCTACAGTGCATCCCTTGTCTGTCTGGTA 781
QY 832 CTTCTTGTCTTGTGTTGCTAGCGGATTAACCCCGGTTCAATTAACAAATCCCTAC 891
DB 782 CTTCTTGTGTTGTTGATGATGTTTAACTTTCCTTCTTCTTCTTCTTCTTCTTCTTCTT 841
QY 892 TTACTTACGTAATCAGGAATTAAGTCTCAATGAGCGCGGTTGGCGAGAACCCCGG 951
DB 842 AAGGCTACGACAAAGTCTCGGCGCATATTATGCTCAATGAGCGCTGTAGTGTGCAACCCG 901
QY 952 TCACCACTACCTAGCGGCTCAACAGCTGCTTTCGACCGCTATTCGCTTAAACCGGCTGA 1011
DB 902 TCACCAACACGCTTCTTCGCTGCGCTGCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCT 961
QY 1012 TATCGGCTCAGTGGAAAGTACCGATGCTCGAAGCGGCTGTAGGCGGTTTCGCGCGGA 1071
DB 962 TAGCAGGCTAATTGGAACGTTATGACGATGCAACCGGACTTCTAGGCGGCTTTCAGCTA 1021
QY 1072 TAACAGCGGTTGCTCCGTTGCTGAGCGCATCGGAGCGCATCGTATGCGGTTTCTGCTT 1131
DB 1022 TAACCTCCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1081
QY 1132 CTATAGTATTAATAGCTTCGCAACAAATTAGCAGAGAGGTTAAGTTTCGACGATCTCTCG 1191

1432 CTTACAGAGGATGAGTTGGGGGATGACATGACTGGCATGAGGCTTTGCTATGCTT 1491
1382 CAGCAGAAGATGAGTGGCAGGAATGGACATGACACGTATGAGGATTTGCTTACGCAT 1441
1492 ATGAGGATGATGA 1504
1442 ACAATGACGAGA 1454

RESULT 10
JS-09-938-842A-1887
Sequence 1887, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
FILE REFERENCE: SCRIPT100-3
CURRENT APPLICATION NUMBER: US/09/938,842A
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,966
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1887
LENGTH: 1497
TYPE: DNA
ORGANISM: Arabidopsis thaliana
JS-09-938-842A-1887

Query Match 41.1%; Score 700.4; DB 9; Length 1497;
Best Local Similarity 69.7%; Pred. No. 2.5e-175;
Matches 995; Conservative 0; Mismatches 421; Indels 12; Gaps 3;
107 GGCCCAACTTCTCGGCCCAACACACAGACGCCCTCGCCGCGCTCCCTTTACTCGGG 166
27 GGCCGATCTCGCCACCTACTTGGGCCCAACGCCACGGCGGGCGGCGGACTACATTGCGG 86
167 CAATTTGCGCGCGGTGGACAGCAAGTTGCTGACACAGGCCCTTCGCGGTCGACACACTA 226
87 CCAATTAGGCACCGTTTAAACAAGTTTCAACGATGACGCTTCCGCCATAGACACACTA 146
227 CTTCTCTTTTCGCGCTACCTCTGTTTTTCTATGACGCTCGGCTTCGCCATGCTCTGGC 286
147 CTTCTCTTTCTGCGCTACTTGTCTTGGCCATGACGCTCGGCTTCGCTATGCTTTGTC 206
287 CGGCTCGGTCGCGCGCAACACCAATGACATCATGTCTCAACAGTCTTCGACGCTGC 346
207 TGGTTCTGTATAGGCCCAAGATACGATGAACATCATGCTTACCAATGCTCTGACGCTGC 266
347 CGCGCGCGCTCTTCTACTCTCTCGGCTTCGCTTTCGCTTCGCTTCGCTCCCTCCAA 406
267 AGCGGAGAGACCTTCTACTATCTTTTGGTTTACGCTTTCGCTTTCGCTTTCGCTTTCG 326
407 CGGCTTCATCGGTAACATTTCTTCGCGCTCAAGACATCCCTTTCATCTCTCTACGACTA 466
327 AGGGTTTCATTGGAAGACACAACTTTGCTCTTACGACTTTCGACTCCCAACAGCTGATTA 386
467 CAGCTACTCTCTACCAATGGGCTTCGCCATCGCGCGCGGCGCATCCAGCGGAAG 526
387 CTCTTTCTCTCTCAATGGGCTTCGCCATCGCGCGCGGCGCTGGAATCAAGTGTGTC 446
527 CATCGCGCAACGACACAGTTCGCTGCTTATCTCATCTACTCTCTCTCTCTCAACGCTT 586
447 GATCGCAGAGAGACTCAGTTCGCTGCTTACTTGTATATACCTCTCTTCTTAAACGGATT 506
587 CGTCTATCCGCTGGTCTCCCACTGCTTCTGGTTCGCCACAGCGCTGGGCTCTGCTTTAA 646

Db 507 TGTTTACCGGTTGCTCTCACTGTTTGGTCCCGATGGATGGCCAGTCCCTTTG 566
Qy 647 GATCAC---CGACCGGCTATTTCCACCGGCTAATAGACTTCGCGGTTCCGCGCTAGT 703
Db 567 TTCAGCGGATGATCGTTTGGTTAGCACCGGAGCCATTGACTTTGCTGCTCCGCTGTGT 626
Qy 704 CCACATGTCGCGGGAATAGCCGCCCTATGGGGAGCGCTGATCGAAGGCCCAAGAATGGG 763
Db 627 TCACATGTCGTTGGTGGCATAGCAGGTTTATGGGGTCTCTTATTGAAGGTCCTCGTCGTG 686
Qy 764 AGTTTCGATCATGACGACGAGCTGGCTTCGAGGGGACACAGCGCTCTTACTAGT 823
Db 687 TCGGTTTCAGAAAGTGTGCGCTATTGCTCTCGCGGCGCACTCTGCTCTGCTAGTGT 746
Qy 824 CTTGGGAACCTTTCTGCTTTGCTTGGTTGCTGAGGATTTAAGCCCGGTTCAATTAACAA 883
Db 747 CTTAGGAACCTTCTCTCTCTGTTGGATGATGTTTCAACCCCGGTTCTTCTACTAA 806
Qy 884 ATCTCTACTTACTTACGGTAACTCAGGAATTAAGTACGCTCAATGAGCGGCTTGGCAG 943
Db 807 GATCTCTGTTCCGTA---TAATCTGTTTCCAACTACGGCCAAATGGAGCGGAATCGGCG 863
Qy 944 AACCCCGCTCACCACTACCTTAGCGGGGTCAAACAGCTGCCCTTGACACGCTATTTCGATA 1003
Db 864 TACAGCGGTTAAACCAACCACTCTCAGGATGCACACAGCTCTAACCACTCTTTGGTAA 923
Qy 1004 ACGGCTGATATCCGCTCACTGGAACGTGACCGATGCTGCAACGGGCTGTAGCGGTTT 1063
Db 924 ACGTCTCTATCAGGCCACTGGAACGTGTAACGGAGCTTTGCAACGGGTTACTCGGTGGTT 983
Qy 1064 CGCGCGGATAACAGCCGCTTCTCCGTGGTTGAGCCATGGCGGAGCCATCGTATGCGGTTT 1123
Db 984 TCGGCGCATTAACCGAGGTTGCTCCGCTGAGGCCATGGCGAGCTTGTGTGCGCTT 1043
Qy 1124 TGTGCTCTTATAGTATTATAGCTTCCAACTTACGAGGATGAGGAGGTTAAGTTCACGA 1183
Db 1044 CATGCTTCTCTGCTCTTATCGGATGCAACAGCTCGCGAGCTTTGTACAATATGATGA 1103
Qy 1184 TCTCTGAGCGCGGCGAGTTGACGCTGCTGGGTGTCGACGCTGGGGGTGATATTCACGGC 1243
Db 1104 TCCACTCGAGCGAGCCCACTACATGAGGCTGTCGCGGTGGCGGTGATATTCGTAGG 1163
Qy 1244 GTTGTTCGAAAAAGAGATGATGAAAGGAGTTTACGG-----GTTGGGAGGCGCA 1297
Db 1164 ATTGTTTCCCAAGAGAAGTATCTAAACGAGGTTTATGGCGCCACCCCGGGAAGCCATA 1223
Qy 1298 CGGCTTGTCTCATGCGGGGTGTCGGAAGTTGTCGGCGGCGACGTCGATTCAGATTCTGT 1357
Db 1224 TGGACTATTTATGGCGGAGGAGGAGGAGCTTTGGGAGCAATTTGGTTCAATATCTGT 1283
Qy 1358 GATTGCTGGGTGTTAGTGCACCATGGAACCCCTTGTTTTGGGGTTGAATAAAGTAA 1417
Db 1284 GATTGAGGATGGGTTAGTGCACCAATGGGAACACTCTTCTTCATCTCAAAAGGCTCAA 1343
Qy 1418 GCTGTTGAGGATTTCTTCAGAGGATGAGCTTGGGGGAGGACATGACTCGCCATGAGG 1477
Db 1344 TCTGCTTAGGATCTCGGAGCGACATGAAATGCAAGGATGGAATGACAGCTCACGGTGG 1403
Qy 1478 CTTTGTCTTATCTTATGAGGATGATGAGCGCAACAGCATGGGATGCA 1525
Db 1404 CTTTGTCTTATCTTACCATGATAATGATGATGATGCTCATAGAGTGA 1451

RESULT 11
US-09-938-842A-1887
Sequence 1887, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong

; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING

; FILE OF INVENTION: SAME, AND METHODS OF USE

; CURRENT APPLICATION NUMBER: US/09/938,842A

; CURRENT FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: US 60/227,866

; PRIOR FILING DATE: 2000-08-24

; PRIOR APPLICATION NUMBER: US 60/264,647

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111

; PRIOR FILING DATE: 2001-06-22

; NUMBER OF SEQ ID NOS: 5379

; SEQ ID NO 1887

; LENGTH: 1497

; TYPE: DNA

; ORGANISM: Arabidopsis thaliana

US-09-938-842A-1887

Query Match 41.1%; Score 700.4; DB 11; Length 1497;
Best Local Similarity 69.7%; Pred. No. 2.5e-175;
Matches 995; Conservative 0; Mismatches 421; Indels 12; Gaps 3;

2y	107	GGCCCACTTCTCGGCCCAACACACAGACGCTCGCGCGCGCTCCCTTATCTGCGG	166
2b	27	GGCGATCTCGCCACCCCTACTTGGCCCAACGCGCGCGCGCGCTACATTTGCGG	86
2y	167	CCATTTCCGCGCGTGACAGCAAGTTCTGCGACAGCGCTTCGCGTGCAGAACACCTA	226
2b	87	CCAATTAGGACACGTTAAACAAAGTTACCGATGAGCGCTTCGCCATAGAACACCTA	146
2y	227	CTCCTCTTTTCGCGCTTACTCTGTTTTTTCTATGACAGCTCGGCTTCGCCATCTCTGCGC	286
2b	147	CTCCTCTTTCTCTGCGCTTACTCTGTTGCGCATGACAGCTCGGCTTCGCTATGCTTTGNC	206
2y	287	CGGCTCGCTCGCGCAAGAACACCATGACATCATGCTCCACAGCTCTGAGCGTGC	346
2b	207	TGGTTCTGTTAGGACCAAGAAATACGATGAACATCATGCTTACCAATGCTCTGAGCGTGC	266
2y	347	CGCGCGCGCTCTTCTACTACCTCTTCTCGGCTTCGCTTTCTGCGTCCCGCTCCAA	406
2b	267	AGCGGAGGACTCTTCTACTATCTCTTGGTTAGCGCTTTCGCTTGGAGGATCTTCCA	326
2y	407	CGGCTCATCGTTAAACATTTCTTCGCTCTCAAGACATCCCTTCTATCTCTCTAGACTA	466
2b	327	AGGTTCTATTGGAAGACACAACTTTGCTCTTAGAGACTTTCCGACTCCCGACAGCTGATTA	386
2y	467	CAGCTACTTCTCTACCAATGGCCCTTCGCCATCGCGCGCGCGCATCACAGCGGAAG	526
2b	387	CTCTTTCTTCTCTACCAATGGCGTTTCGCAATCGCGCGCGTGAATCAAAAGTGGTC	446
2y	527	CATCGCGGAAGCACACAGTTCTGCGCTTATCTCATCTACTCTCTCTCTCTCTCTCTCT	586
2b	447	GATCGCAGAGGACTCAGTTCTGCGCTTACTTGTATATCTCTCTCTCTCTCTCTCTCT	506
2y	587	CGTCTATCGCGTCTCTCCACTGTTCTGCTCCAGACGCTCGGCTCTGCTCTTAA	646
2b	507	TGTTTACCGGTTGTTCTCTACTGTTTGGTTCGCGATGATGAGGCGAGCTCTCTCTCG	566
2y	647	GATCAC---CGACCGCTATTTCCACCGCGCTAATAGACTTCGCGGTTCCGCGTAGT	703
2b	567	TTACGCGGATGATCGTTTCTTTAGCACCGGAGCCATTGACTTTGCTGCTCGGTTGT	626
2y	704	CCACATGTTCCGCGGAATAGCGGCTATGGGAGCGGTGATCGAAGCCCAAGATGGG	763
2b	627	TCACATGGTTGGGCAAGAGGTTTATGGGCTGCTCTTATGAGGCTCTCTCTCTCTCT	686
2y	764	ACGTTTCGATCATGACGAGCAGCTGTGCGCTTCGAGGCCACAGCGCTCTCTTAGTAGT	823
2b	687	TCGGTTTCGAGAAAGGTGGTTCGCGCTATTGCTCTGCGCGGCCACTCTGCTCGCTAGTAGT	746
2y	824	CTTGGGAACCTTCT	883
2b	747	CTTAGGAACCTTCT	806

Qy	884	AATCTTACTTACTTACGGTAATCTCAGGAATTTACTACGGTCAATGAGCGCGTTGGCAG	943
Db	807	GATCTCTGTTCCGTA---TATCTGTTCCAACTACGCGCAATGAGCGGAATCGGCGG	863
Qy	944	AACGGGTCACACACTTACCCCTAGCGGGTCAAACAGCTGCTTTGACACAGCTATTCCGTAA	1003
Db	864	TACAGGGTTAAACACACACTCTCAGGATGACAGCAGCTCTTAACACACTCTTTGGTAA	923
Qy	1004	ACGGGTGATATCCGGTCACTGAAAGTGCAGCATCTCTGCAACGGGCTTTAGGCGGTT	1063
Db	924	ACGTCTCTATCAGGCCACTGGAACGTAAACGAGCTTTGCAACGGGTTACTCGGTGGGT	983
Qy	1064	CGCGCGATAACACAGCGGTTGCTCCGTGTTGAGCCATGGGCGAGCATCTGATCGGTTT	1123
Db	984	TGCGGCGATAACCGCAGGTTGCTCCGTGATGAGCATGGGCGAGGATTGTGTGCGGCTT	1043
Qy	1124	TGTTGCTTCTATAGTATTAATAGCTTGCACAAATTAAGACAGAGGTTAATTCGACGA	1183
Db	1044	CATGGCTTCTGCTGCTTATCGGATGCAACAGCTCGCGAGCTTGTACAAATATGATGA	1103
Qy	1184	TCCTCTGAGGGCGCGCAGTTGCAAGCTGGGTGTGGCACGCTGGGGGGTGAATTCACGCG	1243
Db	1104	TCCACTCGAGGCGAGCCCACTACATGAGGGTGTGGCGGTGGGGTTGATATTCTGTAAG	1163
Qy	1244	GTGTTTCGCAAAAAGGAGTATGTGAAGAGGTTTACCGG-----GTTGGGAGGGCGCA	1297
Db	1164	ATTGTTTGCACAAAGAGAGTATCTAAACGAGGTTTATGGCGCCACCCCGGAGGCCATA	1223
Qy	1298	CGGTTTGTCTCATGCGGGGGTGGTGGGAAGTTGCTGGCGCGCACGCTGATTCAGATTCTGGT	1357
Db	1224	TGGACTATTATTAGGCGGAGGAGGAGCTGTGTTGGAGCACAAATTGGTTCAATACTTGT	1283
Qy	1358	GATTGCTGGTGGGTTAGTGCACCATGCGACCTTGTGTTGGGGGTTGAAATAAAGTAA	1417
Db	1284	GATTGAGGATCGGTTAGTGCACCAATGCGGAACTCTTCTTCTCATCTCAAAAGGCTCAA	1343
Qy	1418	GCTGTTGAGGATTTCTTCAGAGGATGAGCTTTCGCGGATGACATGCTCGCCATGGAGG	1477
Db	1344	TCGCTTAGGATCTCGAGCAGCATGAATGCAAGGATGATATGACACGTCACGTCAGGTGG	1403
Qy	1478	CTTGTGTTATGCTTATGAGGATGATGAGACCGCACCAAGCATGGGATGCA	1525
Db	1404	CTTGTCTATATCTACCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	1451

RESULT 12

US-10-424-599-70091

; Sequence 70091, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 70091

; LENGTH: 842

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_34303C.1

US-10-424-599-70091

Query Match

Best Local Similarity 28.6%; Score 488.2; DB 12; Length 842;

Matches 538; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 1006 GGGTATATCCGGTCACTGGAAAGTACCGATGCTGCAACGGGCTGTAGCGGTTTCG 1065
DB 1 GGATGATATCCGGTCACTGGAAAGTACCGATGCTGCAACGGGCTGTAGCGGTTTCG 60
QY 1066 CGGCGATAACAGCGGTTTCCTCGTGGTGGAGCCATGGCAGCCATCGATGCGGTTTCG 1125
DB 61 CGGCGATAACAGCGGTTTCCTCGTGGTGGAGCCATGGCAGCCATCGATGCGGTTTCG 120
QY 1126 TTGCTTCTATAGTATTAAATAGTTCGAAACAAATAGCAGAGAGGTTAAGTTCGACGATC 1185
DB 121 TCGCTTCAGTGGTTCGATAGCGTGCACAAATAGCAGAGAGGTTAAGTTCGATGATC 180
2Y 1186 CTCTGGAGGCGGCGCAGTTCACAGTGGGTGGCAGTGGGGGGTGTATATTCAGCGGT 1245
DB 181 CTTTGGAGGCGGCGCAGTTCACAGTGGGTGGCAGTGGGGGGTGTATATTCAGCGGC 240
2Y 1246 TGTTCGCAAAAAGGAGTATGTGAAGAGGTTTACCGGTTGGGAGGCGCAGCGGTTGC 1305
DB 241 TGTTCGCAAAAAGGAGTATGTGAAGAGGTTTATGGGAGGCGCAGCGGTTGT 300
2Y 1306 TCATGGGGGTGTGGAGTTCCTGGCGCGCAGCTGATTCAGATTCGTGATGCTG 1365
DB 301 TCATGGGGGTGTGGAGTTCCTGGCGCGCAGCTGATTCAGATTCGTGATGCTG 360
2Y 1366 GGTGGGTAGTGGCAGCAGTGGACCTCTGTTTGGGGTGTGAATAAAGTGAAGCTGTTGA 1425
DB 361 GGTGGGTAGTGGCAGCAGTGGACCTCTGTTTGGGGTGTGAATAAAGTGAAGCTGTTGA 420
2Y 1426 GATTTCTTCAAGGATAGCTTGGGGGATGACATGATCGCATCGGAGGCTTGTGCT 1485
DB 421 GATTTCTTCAAGGATAGCTTGGGGGATGACATGATCGCATCGGAGGCTTGTGCT 480
2Y 1486 ATGCTTATAGGATGATGACACCAAGCATGGGATGAGTTCAGTGGAGGTTGGGCCA 1545
DB 481 ATGCTTATAGGATGATGAGTTCAGACCAAGCATGGGATGAGTTCAGTGGAGGTTGGGCCA 540
2Y 1546 ACGGCTTCTCCACCCACCACTGATGAATGATTTTTTCCCATATGCAATGCTCANT 1605
DB 541 ACGGCTTCTCCACCCACCACTGATGAATGATTTTTTCCCATATGCAATGCTCANT 600
2Y 1606 AGTCAACATTAATTTGAT 1626
DB 601 AGTATATCTTCAATGAAT 621

RESULT 13
JS-10-425-114-32362
; Sequence 32362, Application US/10425114
; Publication No. US20040034898A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 32362
; LENGTH: 1498
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-ZMFLB73301E06_FLI
JS-10-425-114-32362

Query Match 27.5%; Score 469; DB 12; Length 1498;
Best Local Similarity 69.9%; Pred. No. 7.3e-114;
Matches 647; Conservative 0; Mismatches 275; Indels 3; Gaps 1;

QY 583 GCTTGTCTATCCGGTGTCTCCCACTGCTTCTGTCGCCAGAGCGCTGGGCTCTCCT 642
DB 1 GCTTGTCTATCCGGTGTCTCCCACTGCTTCTGTCGCCAGAGCGCTGGGCTCTCCT 60
QY 643 TTAAGATCACCGACCGGTATTTTC---ACCGCGTAATAAGATTTCCCGGTTTCGCG 699
DB 61 GCGGACGCTCCGCGCGCTGCTCTTCGGGTCCGCGCTCATCGACTTCGCGGCTCCGCG 120
QY 700 TAGTCCACATGTCGCGGAAATAGCCGCTATAGGGAGCGCTGATGAAAGGCCCAAGAA 759
DB 121 TGTTCACATGTCGCGGCAATCGCGGCTGTGGGCGCTCATCGAGGCCCCCGCA 180
QY 760 TGGAGCTTTGATCATCAGAGAGCTGTGGCTTTCGAGGCCACAGCGCTTCCTTAG 819
DB 181 TCGGCGCTTTCACACCGCGCGCTCCGTGGGCTCAAGGGCCACAGCGCTCGCTCG 240
QY 820 TAGTCTCGGAGACCTCTGCTTGGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGGTTC 879
DB 241 TGTGCTCGGACCTCTGCTTGGTTCGGTTCGGTTCGGTTCGGTTCGGTTCGGTTC 300
QY 880 ACAAATCCTACTTACTTACGGTAACTCAGGAAATTAACGCTCAATGGAGCGCGTTG 939
DB 301 CCACCATCTCAAGTCGTACGCGCGCGCGGACCGTCCACGGGCTGCTCGCGCTG 360
QY 940 GCAGAACGCGGTACCACTACCTAGCGGCTCAACAGCTGCTGCAACGGGCTGTAGCG 999
DB 361 GCGGACCGCGCTACCACTACCTAGCGGCTCAACAGCTGCTGCAACGGGCTGTAGCG 420
QY 1000 GTAAACGGGTGATATCCGCTCACTGGAACGCTGACGATGCTGCAACGGGCTGTAGCG 1059
DB 421 GGAAGCGGCTCCAGACGGGCTCACTGGAACGCTGGAACGCTGCAACGGGCTCTCGCG 480
QY 1060 GTTTCGCGGATACAGCGGTTGCTTCCGTTGAGCTTGGCCATGGGAGCCATCGTATGCG 1119
DB 481 GGTTCGCGGATACAGCGGTTGCTTCCGTTGAGCTTGGCCATGGGAGCCATCGTATGCG 540
QY 1120 GTTTCGTTCTTATAGTATTAATAGCTTGCACAAATAGCAGAGAGGTTAAGTTTCG 1179
DB 541 GGTTCGTTCTTATAGTATTAATAGCTTGCACAAATAGCAGAGAGGTTAAGTTTCG 600
QY 1180 AGATCTCTTGGAGCGCGGCTGCTGACGTTGCTGAGTGGGTGGCCATGGGAGGTTATTC 1239
DB 601 ACGACCGCTGGAGCGCGGCTGCTGACGTTGCTGAGTGGGTGGCCATGGGAGGTTATTC 660
QY 1240 CGCGGTTGTTCCAAAAAGGAGTATGTAAGAGGTTTACGGGTTGGGAGGCGCGCAG 1299
DB 661 CGGGCTCTTCCGAGGCGGAAAGTACGTTGAGAGAGATCTACGGCGCGGAGGCCCTACG 720
QY 1300 GGTTCGTCATGCGGCGGTGGTGGAGTTGCTGGCGGCGCAGTGAATTCAGATTCGTGTA 1359
DB 721 GGTTCGTCATGCGGCGGTGGTGGAGTTGCTGGCGGCGCAGTGAATTCAGATTCGTGTA 780
QY 1360 TTGCTGGGTGGGTAGTCCGACCATGGACCTGTTGTTGGGGGTTGAATAAAGTGAAG 1419
DB 781 TCGCGGCTGGGTGAGTGGACCATGGCCGCTCTTCTACGCGCTCAAGAGCTGGGCC 840
QY 1420 TGTGAGGATTTTCAGAGGATGAGTTCGGGGATGAGCATGATTCGCGCATGGAGGCT 1479
DB 841 TGTGCGCATCTCGGCGGACGACGAGATGTCGCGCATGGACCTGACCCGCGCAGCGCGCT 900
QY 1480 TTGCTTATGCTTATGAGGATGATGA 1504
DB 901 TCGCTACGCTACCAACGACGAGGA 925

RESULT 14
US-10-424-595-109084
; Sequence 109084, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K

RESULT 15
 S-10-424-599-139607
 Sequence 139607, Application US/10424599
 Publication No. US20040031072A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa Thomas J
 APPLICANT: Kovalic David K
 APPLICANT: Zhou Yihua
 APPLICANT: Cao Yongwei
 TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53223)B
 CURRENT APPLICATION NUMBER: US/10/424,599
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 285684
 SEQ ID NO 139607

Search completed: March 9, 2004, 16:03:09
Job time : 1300 secs

SEQ ID NO 139607

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2004, 10:35:31 ; Search time 4638 Seconds
(without alignments)
10984.235 Million cell updates/sec

Title: US-10-033-109-3
Perfect score: 1706
Sequence: 1 gacagagactcccaaccc.....aaaaaaaaaaaaaaaaaaaaa 1705

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_estci:*
9: gb_estcl:*
10: gb_estc2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	512.4	30.0	986	14	CK251554 EST735191
2	490.8	28.8	795	14	CD575822 UCRPT01_0
3	489.8	28.7	836	29	CC722552 OGVBU66TV
4	485.6	28.5	970	14	CK263329 EST709407

C	5	485.4	28.5	775	29	CG219364	CG219364
	6	483.8	28.4	941	14	CK290978	EST7753692
	7	482.4	28.3	968	14	CK282541	EST745263
	8	481.4	28.2	925	14	CK290394	EST753108
	9	474	27.8	970	14	CK289847	EST752569
	10	463	27.1	971	14	CK287788	EST750510
	11	460.2	27.0	975	14	CK294612	EST757326
	12	453.8	26.6	961	14	CK285989	EST748711
	13	451.4	26.5	722	29	CG745155	ZMMBB012
	14	443.2	26.0	847	10	BE998772	EST7430559
	15	437.6	25.7	984	14	CK280628	EST743350
	16	436	25.6	927	14	CK290587	EST753301
	17	433.2	25.4	962	14	CK295232	EST757946
	18	429	25.1	954	14	CK294795	EST757509
	19	428.4	25.1	815	14	CB895201	EST7647993
	20	424.8	24.9	866	14	CF207646	CAB20002
C	21	422.2	24.7	703	29	CG263379	OG0BT15TV
	22	421.8	24.7	949	14	CK288020	EST750742
	23	419.4	24.6	706	14	CA781520	022G09AF
C	24	418.8	24.5	926	14	CK282540	EST745262
	25	418	24.5	913	14	CK286736	EST749458
	26	417	24.4	860	14	CK282387	EST745109
	27	416.6	24.4	858	14	CK294296	EST757010
	28	415.4	24.3	765	12	BG645673	EST507292
	29	415	24.3	865	14	CK298495	EST761209
	30	411.8	24.1	796	29	CG438838	OGVGE86TH
	31	409	24.0	777	14	CB619922	OSTIE304M
	32	408.6	24.0	739	29	CG220307	OGAW88TH
	33	407.8	23.9	909	14	CK298198	EST760912
C	34	403.8	23.7	770	14	CB891201	EST7648170
	35	403.6	23.7	971	14	CK282386	EST745108
	36	403.2	23.6	884	14	CK294339	EST757053
	37	403.2	23.6	927	14	CK279062	EST725140
	38	402.6	23.6	804	28	B2529693	OGAJO39TC
	39	401.8	23.6	779	14	CB892609	EST7645401
	40	398.8	23.4	842	14	CK280629	EST743351
	41	395.2	23.2	602	9	AU089425	AU089425
	42	390	22.9	913	14	CK261120	EST707198
C	43	383.8	22.5	822	14	CK291607	EST754321
	44	377.4	22.1	853	14	CK097232	UB44DFC08
	45	374	21.9	690	14	CD861700	AZ01_003G

ALIGNMENTS

RESULT 1
CK251554
LOCUS
DEFINITION
EST735191 potato callus cDNA library, normalized and full-length
Solanum tuberosum cDNA clone POC8035 5' end, mRNA sequence.
ACCESSION
CK251554
VERSION
CK251554.1 GI:39804693
KEYWORDS
EST.
SOURCE
Solanum tuberosum (potato)
ORGANISM
Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
REFERENCE
1 (bases 1 to 986)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
JOURNAL
COMMENT
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

Location/Qualifiers
1. 986
/organism="Solanum tuberosum"
/mol_type="mRNA"

Db	857	CGGGTTTAAACCGGGTTTCATTATATAAATCTAAATTACTTACGACGGTCAACCGGAGG	916
Qy	914	TTTACTACGGTCAATGGAGCGCGGTTGTCAGAAACCGGGTACCACCTACCTACGCGGTC	973
Db	917	GTATTATGGTCAATGGAGCGGTTGAGGCCGAACCGCGGTTACAACTACCCCTAGCCGGTTG	976
Qy	974	AACAGCTGCC	983
Db	977	CACCGCGGCC	986

Query Match	30.0%; Score 512.4; DB 14; Length 986;
Best Local Similarity	72.0%; Pred. No. 5e-47;
Matches 698; Conservative 0; Mismatches 266; Indels 6; Gaps 2;	
2Y	17 CCCCACCCGCTAGTTTCTACCACCTTCAGTCACGGCGTAATACATCAACCAACCCACCCCTCTCACGCCACCCCCACCCCAT 76
bB	20 CTCGCCITCTTCTCCTTACCCACCCACCCCTCTCACGCCACCCCCACCCCAT 79
2Y	77 GTGCGTGCTGTGTTCCCGCGGAACAACCTGGCCCAACTTCTCGSCCCAAACACCAAGA 136
bB	80 CAGCCCAATGCTGTGTTCCGTCGATACACTCGCTCCGTTCTCTCGTCCCAACACCAACCAA 139
2Y	137 CGCTCCGCSCGCGCTCCCTTATCTGCGGCATTTCGCGCGCGTGGACAGCAAGTTCGT 196
bB	140 GCCGTGCGCCGCCCTCFATCATCTGAACCAATTTCCGCTGTATCGGACAGATTCTGT 199
2Y	197 GCACACGCGCTTCGCCGTGCACAACACTACTCTCTTTTCGCGCTACTCTCGTTTTTTC 256
bB	200 CGATAACCGTTATGCAATCGATACCAATATCTCTCTCTCAGCTTATCTCGTTTTCTC 259
2Y	257 TATGCAGCTCGGCTTCGCCATGCTCTGCGCGGCTCCGTCGCGCCAAGAACACCATGAA 316
bB	260 TATGCAGCTCGGTTTCGTATGCTTTCGCGGGCTCTGTCCGTGCAAGAATACAATGAA 319
2Y	317 CATCATGCTCAACAACTGCTGTGAACGCTGCGCGCGCGGCTCTTCTACTACCTCTTCGG 376
bB	320 CATCATGCTTACAAATGTCCTGATGCTGCGCGGCTGGACTTTTCTATTACCTATTCCG 379
2Y	377 CTTCGCGCTTCGCTTCGGCTCCCGCTCCCAAGCGGCTTCATCGGTAAACAATTTCTTCGGCT 436
bB	380 ATTTCGCTTCGCTTCGGGCGGTCGCTCTAATGGATTTCATCGGCCGACATTTCTTCGGGCT 439
2Y	437 CAAGGACATCCCTTCATCTCTACGACTACAGCTACTTTCCTCTACCAATGGGCTTCGC 496
bB	440 TAAGAGATCCGTCAAATTCATTTCGATTACAGTAATTTCTCTATCATGGGCTTCGC 499
2Y	497 CATCGCGCGCGCGCATACCAAGCGAAGCATTCGCGGAACGCAACAGTTCTGGGCTTA 556
bB	500 CATCGCGCGCGCGGTATCAACAGCGGTTCAATCGCGCAACGCAACCAATTTGTGGGCTA 559
2Y	557 TCTCATCTACTCTCTTCCTCAACGCTTCGTCATCCGCTGCTCCCACTGCTGCTG 616
bB	560 TTGTGATTTATCTCTTTCTAACCGGTTTCGTTACCGCGTTGATCTCATTTGGTTTG 619
2Y	617 GTCCCCAGACGGCTGGGCTCTGCTTTAAGATCACCGACCGGCTATTTCACCGCGGT 676
bB	620 GTCCCCAGATGGGTGGGCTAGCCCGGGTAA---TTCAAATCTTTTATTCGATCCGGTGT 676
2Y	677 AATAGACTTCCCGGTTCCGCGGTAGTCACATGCTCGCGGAATAGCGGCTATGGG 736
bB	677 TATCGATTTCCCGGGTGGGTGTAGTTTCATGTAGGTGGAAATGCGGGTTTATATGG 736
2Y	737 AGCGCTGATCGAAGGCCCAAGAATGGGACGTTTTTCGATCATGCAGGACGAGCTGTGGCCTT 796
bB	737 AGCTTTAATTGAAGGTCCGAGAAATCGGCGGTTTCGATCATACGGTTCGATCCGTTGCACT 796
2Y	797 GCGAGGCCACAGCGGCTCTTAGTAGTCTGGGAACCTTCTTGCTTTGGTTGGTTGGTA 856
bB	797 TCGTGGACATAGCGGCTCACTCGTGGTCTTAGGCACCTTTTATTATGGTTCGATGGTA 856
2Y	857 CGGATTTAACCCCGGTTTCATTTAACAAAATCTCTACTTACTT---ACGGTAACTCAGAAA 913

LOCUS	CD575822	795 bp	mRNA	linear	EST 12-JUN-2003
DEFINITION	UCRPT01_0laf10_g3 <i>Poncirus trifoliata</i> CTV-challenged cDNA library - AGI <i>Poncirus trifoliata</i> cDNA clone UCRPT01_0laf10, mRNA sequence.				
ACCESSION	CD575822				
VERSION	CD575822.1				
KEYWORDS	EST.				
SOURCE	Poncirus trifoliata				
ORGANISM	Poncirus trifoliata				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosids; eurosids II; Sapindales; Rutaceae; Poncirus.				
AUTHORS	1 (bases 1 to 795) Roose,M.L., Ye,X., Federici,C.F., Close,T.J., Fenton,R.D., Wanamaker,S., Collura,K., Feuerbacher,O., Kim,H.R., Kudrna,D., Wing,R. and Yu,Y.				
TITLE	Development of EST Resources and New Genetic Markers for California Citrus - <i>Poncirus trifoliata</i> CTV-challenged phloem - AGI				
JOURNAL	Unpublished (2003)				
COMMENT	Contact: Mikeal Roose Department of Botany & Plant Sciences, University of California Riverside, CA, 92521-0124, USA Tel: 9097874137 Fax: 9097874437 Email: mikeal.roose@ucr.edu Seq primer: T3.				

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Location/Qualifiers
1. .795
/organism="Poncirus trifoliata"
/mol_type="mRNA"
/cultivar="Pomeroy Op"
/db_xref="taxon:37690"
/clone="UCRPT01.01a10"
/tissue_type="Phloem"
/dev_stage="10 - 30 cm shoots"
/lab_host="E. coli TUC121"
/clone_lib="Poncirus trifoliata CTV-challenged cDNA
library - AGI"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site 1: EcoRI; Site 2: XhoI; Plants were grown in the
greenhouse at University of California, Riverside. The
scion was open-pollinated (very probably selfed)
seedling of Poncirus trifoliata cv Pomeroy that was
selected as homozygous for the Ctv resistance gene. The
rootstock was sweet orange infected with citrus tristeza
virus (CTV) isolate T14 over 1 year before sampling (Ctv
infects sweet orange, but not genotypes carrying the Ctv
resistance gene. Shoots 10-30 cm long were harvested in
October 2000, and the green phloem (bark) was removed and
frozen quickly in dry ice. Total RNA was extracted using
TriZol reagent (Gibco). Poly(A) RNA was purified, a cDNA
library was made, and 0.5 million primary lambda cDNA
clones were in vivo excised to give a population of
pBluescript SK(-) phagemids. All steps to this point were
performed in the M.J. Roosa lab at the University of
California, Riverside by X. Ye. Phagemids were plated,
plasmid DNA purified, cDNA clones archived, and DNA
sequences determined bi-directionally using an ABI3730 at
the Arizona Genomics Institute, University of Arizona
(Collura, Feuerbacher, Kim, Kudrna, Wing, Yu).

```

Chromatogram files were transmitted to UC Riverside. (by yul), then processed at UC Riverside (by Wanmaker) using the Harvest pipeline (http://harvest.ucr.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region. Sequences that retained a phred 17 region of at least 100 bases were deposited to GenBank."

ORIGIN

```
Query Match      28.8%; Score 490.8; DB 14; Length 795;
Best Local Similarity 81.2%; Pred. No. 1.2e-44;
Matches 570; Conservative 0; Mismatches 132; Indels 0; Gaps 0;

2y 89 TTGTCCCGCGGAACTGGCCCAACTTCTCGGCCCAACACACAGAGCGCTCCGCGC 148
2b 78 TTGTTACGGGAGCTACTCGCGGCTTCTTGCCGCCAAGCCACCAAGCGCTCTGTCAGC 137
2y 149 CGCTCTCTTATCTCGGGGCAATTTCCGCGCGGFGACAGCAAGTTCTGTCGACAGCGCTT 208
2b 138 AGCTCTCTTAATCTGCTCCCAACTCGAAGCCATCAACAATAAGTTTCCGACACCGCAT 197
2y 209 CGCGGTGCAACACACTACTCTCTCTTTCCGCTACCTCGTTTCTATGACGCTCG 268
2b 198 CGCGGTGCACTCACTACTCTCTCTTCCGCTACTTAGTCTTCTCCATGCACTCG 257
2y 269 CTTGCGCATGCTCTGCGCGGCTCGTCCGCGCAAGAACACCATGAACATCATGCTCAC 328
2b 258 CTTGCGCATGCTCTGCGCGGCTCGTCCGCGCAAGAACCATGAACATCATGCTCAC 317
2y 329 CAACGTCTTGAGCGCTGCGCGGCGCTCTTACTACTCTTCGCTTCGCTTCGCTTCGC 388
2b 318 CAACGTCTTGAGCGCGCTGCGCGGCGCTCTTACTACTCTTCGGAATTCGCTTCGC 377
2y 389 TTTCGCTCTCCCTCCCAACGGCTTCATCGGTAAACATTTCTCGGCTTCAAGGACATCCC 448
2b 378 CTTGCGCACCCCTTCTACGGCTTCATCGCGCGCCACAACTTTCGCTTCAAGTCTTCCC 437
2y 449 TTCTATCTCTAGGACTAGCTACTTCTCTACCAATGGGCTTCGCCATCGCGCGC 508
2b 438 CACTCTCAACTTCGACTAGCTACTTCTTACCAATGGGCTTCGCCATCGCGCGC 497
2y 509 CGGCATCAGCAGCGGAAGCATCGCGAAGCACACAGATTCTGTTGGCTATCTCATCTACTC 568
2b 498 CGGCATCAGCTCGGCTCCATCGCGAGCGCACCCAGTTCTGCGCTACTTAACTACTC 557
2y 569 CTCCTTCTTACCGGCTTCTATTCGGTGTCTTCCACTTGTCTGGTCCCGACGCG 628
2b 558 CTCCTTCTTACCGGCTTCTATTCGGTGTCTTCCACTTGTCTGGTCCCGACGCG 617
2y 629 CTGGGCTCTGCTTTAAGATCACCGACCGGCTATTTTCCACCGCGCTAATAGACTTCG 688
2b 618 CTGGGCTAGGCTCCCAACACCGGACCTCTTGTTCGGCTCCGGGCTATCGACTTCG 677
2y 689 CGGTTCCGGGTAGTCCCATGATGGTGGGGAATAGCGGCTATGGGAGCGCTGATCGA 748
2b 678 CGGCTCCGGGTAGTCCCATGATGGTGGGGAATAGCGGCTATGGGAGCGCTGATCGA 737
2y 749 AGSCCAAGATGGGAGCTTCGATCATCGAGGAGAGCTGT 790
2b 738 AGTCCCAAGATCGGAGCTTCGATCATCGAGGAGCTGT 779
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RESULT 3
CC722552/c
OCUS
DEFINITION
  OGBV66TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZM58Ma0498L12,
  genomic survey sequence.
CCESION
  CC722552
VERSION
  CC722552.1 GI:32141485
FEATURES
  ORIGIN
    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 836)

Whitehead, C.A., Quackenbush, J., Van Aken, S., Uterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.

Consortium for Maize Genomics

Unpublished (2002)

Other_GSSs: OGBV66TH

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1. 836

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZM58Ma0498L12"

/clone_lib="ZM 0.7 1.5 KB"

/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN

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Query Match      28.7%; Score 489.8; DB 29; Length 836;
Best Local Similarity 75.3%; Pred. No. 1.6e-44;
Matches 624; Conservative 0; Mismatches 202; Indels 3; Gaps 1;

QY 301 CCAAGAACACCATGAACATCATGCTCACACGCTCGTGGAGCTGCGCGGCGCTCT 360
Db 832 CCAAGAACACCATGAACATCATGCTCACACGCTCGTGGAGCTGCGCGGCGCTCT 773
QY 361 TCTACTACTCTTTCGGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTC 420
Db 772 TCTACTACTCTTTCGGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTC 713
QY 421 ACATTTCTTTCGGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT 480
Db 712 GGCATTTCTTTCGGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT 653
QY 481 ACCAATGGGCTTCGCCATTCGCCCGCGCGCATCACAGCGGAAGCATCGCGAAGCGCA 540
Db 652 ACCAGTGGGCTTCGCCATTCGCCCGCGCGCATCACAGCGGCTCCATCGCGAGAGGA 593
QY 541 CACAGTTCTGCGCTTATCTCATCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 600
Db 592 CCAAGTTCTGCGCTTATCTCATCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 533
QY 601 TCTCCCATCTGTTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 660
Db 532 CGTCCCATCTGTTCTGTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 473
QY 661 TATTTTCC---ACGGCGTATAGACTTTCGCGGTTTCGCGGCTAGTCCATCATGGTGG 717
Db 472 TGCTCTTTCGGTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCTTTCGCGGCT 413
QY 718 GAATAGCGGCTTATGGGAGCGCTGATCGAAGCGCCCAAGAAATGGGAGCTTTCGATCATG 777
Db 412 GCATCGCGGCTTCTGCGGCGCGCTTCTGCGGCGCGCTTCTGCGGCGCGCTTTCGACACG 353
QY 778 CAGGACGAGCTTGTGGCTTTCGAGGCGCACAGCGGCTCTTCTTCTTCTTCTTCTTCTTCT 837
Db 352 CCGCGCGCTTTCGAGGCTTTCGAGGCGCACAGCGGCTCTTCTTCTTCTTCTTCTTCTTCT 293
QY 838 TGCCTTGGTTCGGTTCGAGGATTTAAACCCCGCTTCAATTAACAAATCTTACTTACTT 897
Db 292 TGCCTTGGTTCGGTTCGAGGATTTAAACCCCGCTTCAATTAACAAATCTTCAATCTTCA 233
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898 ACCTAATCTCAGGAAATTAATAGGTCTAATGAGCGCGGTGGGAGAACCGCGGTACCA 957
 232 ACAGCCCGCCCGGACCGTCCACGGGCAATGTGTGCGCGGTGGCGCGCACCGCGGTACCA 173
 958 CTACCTAGCGGGGTCAACAGCTGCTTGACACAGCTATTGCGTAAACGGGTGATATCCG 1017
 172 CCACCTTCGCGGCGAGCGTCCGCGGCTGACCAACGCTGTTGGGAGCGGTCCAGCGG 113
 1018 GTCACTGGAACTGACCGATGTCTGACAGCGGCTTTAGGGCGTTTCGCGGATACAG 1077
 112 GCACCTGGAACTGCTGGAGCTGTGCAACGGGCTCTCGCGGGTTCGCGGCAATCAGG 53
 1078 CCGGTTGCTCCGTTGAGTCAGCATGGGAGCGCATGATGCGGTTTGT 1126
 52 CCGGTTGAGCGTGTGTGAGCGGTGGCGCGCTGCTGTGCGGTTGT 4

RESULT 4

K263329

OCUS

DEFINITION

EST709407 potato abiotic stress cDNA library linear EST 12-DEC-2003

clone POABL79 5' end, mRNA sequence.

CK263329

CK263329.1 GI:39820307

EST.

SOURCE

ORGANISM

Solanum tuberosum (potato)

Eukaryota;

Eukaryota;

Spermatophyta;

Magnoliophyta;

eudicotyledons;

core eudicots;

asterids;

lamids;

Solanaceae;

Solanum.

1 (bases 1 to 970)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.

Generation of ESTs from abiotic stressed potato tissue

Unpublished (2003)

Other ESTs: EST709408

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

Location/Qualifiers

1..970

/organism="Solanum tuberosum"

/mol_type="mRNA"

/cultivar="Kennebec"

/db_xref="taxon:4113"

/clone="POABL79"

/tissue_type="abiotic stress treated leaf and root tissue"

/lab_host="DH10B-TonA"

/clone_lib="potato abiotic stress cDNA library"

/note="Vector: pCMVSPORT6.1; Site_1: EcoRI; Site_2: NotI;

supplier: Solanum tuberosum var. Kennebec plants were

grown from cuttings on a 16hr light/8 hr dark cycle at 25

C for 3-4 weeks. Abiotic stress conditions were applied to

four separate sets of plants. Set 1 involved saturation of

the soil with 150 mM NaCl and tissues were harvested at

following application of the salt stress (leaves: 2hr,

6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, 1d,

2d. Set 2 were grown under the standard conditions and then

were water stressed by withdrawal of further watering

applications. Drought stressed plants were harvested after

cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d

and 5d). Set 3 were grown under the standard conditions

and then were cold stressed by placement at 4 C. Cold

stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,

and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d,

2d. Set 4 were grown under the standard conditions and

then were heat stressed by placement at 35 C. Heat

stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d,

2d and 4d and heat-stressed roots were harvested at 6 hr,

12 hr, 1 d, and 4d. RNA was isolated from all tissues and

equal RNA from each tissue and stress was pooled to

ORIGIN

Query Match
 Best Local Similarity 28.5%; Score 485.6; DB 14; Length 970;
 Matches 668; Conservative 71.5%; Pred. No. 4.2e-44;
 Mismatches 259; Indels 7; Gaps 2;

construct the cDNA library. RNA sample."

17 CCCCACCCGCTAGTTTACCACTTCAGTCAAGCGGTAAATACACTAAACACCCACCAT 76
 29 CTCGCCCTTTCTTCTTACACCCACCCCGCTCTACCCCGCCACCCCGCCAC 88
 77 GTCGCTGCTCTTGTCCGCGGAAACAACTGGCCCAACTTCTCGGCCAAACACACAGA 136
 89 CAGCCCAATGCTTGTTCGCTCGATACATCTCGCTCCGCTCCGCTCCCAACACCAA 148
 137 GCGCTCCGCGCGCTCCCTTATCTGGGCGCATTTTCGCGCGCTGGAGCAGAGTTTCT 196
 149 GCGCTCCGCGCGCTCTATACATCTGCAACCAATTTTCGCGGTGTATCGGACAGATCG 208
 197 CGACACGGCTTCGCGCTCGACCAACCTACCTCTCTTTTTCGCTCTACCTGTTTTTC 256
 209 CGATACCGGTTATGCAATCGATACCAATATCTCTCTTTTTCAGCTTATCTCGTTTCT 268
 257 TATGAGCTCGGCTTCGCGCTTCGCGCGCTGCTGCGCGCGCTGCTGCGCGCAAGAA 316
 269 TATGAGCTCGGTTTCGCTATGCTTTCGCGCGCTGCTGCGCGCGCTGCTGCGCGCAAGAA 328
 317 CATCATGCTCACCAACGCTCTGGAAGCTGCGCGCGCGCTCTCTTCTACTCTCTTCG 376
 329 CATCATGCTTCAAAATGCTCTGATGCTGCGCGCGCTGAGACTTTTCTATCTATCTCG 388
 377 CTTGCGCTTCGCTTTTCGCGCTCCCTCTACGCTTCTCTCTCTCTCTCTCTCTCTCT 436
 389 ATTGCTTTCTGCTTTGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 448
 437 CAAGGACATCT 496
 449 TAAAGAGATCCCGTCAAAATTCATTCGATACAGTAATTTCTCTATCAATGGGCTTC 508
 497 CATCGCGCGCGCGCTATCACAGCGGATCGCGGAGCATCGCGGAAACGACAGTTCTG 556
 509 CATCGCGCGCGCGGTATCACAGCGGTTCAATCGCGGAAACGACCAATTTGTGCGCT 568
 557 TCTCATCTACT 616
 569 TTTGATTTATCT 628
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 629 GTCCCGCAGATGGTGGGCTAGCCCGGTAA--TTCAATCTTTTATTCGGATCCGGTGT 685
 677 AATAGACTTGGCGGTTCCGCGGTAGTCCATGTTGCGCGGATAGCGGCTATGGGG 736
 686 TATCGATTTGCGCGGTCGCGGTAGTTCATGTTAGTGGGATTTGCGGGTTTATGG 745
 737 AGCGTGTATCGAAGCGCCCAAGATGGGACGTTTTCGATCATGAGGACGAGCTGTGCGCT 796
 746 AGCTTTAATTGAAGTCCGAGATCGCGGCTTCGATCATACGGGTTCGATCCGTTGCACT 805
 797 GCGAGGCGCACAGCGGCTCTCTAGTTCCTGGGAAACCTTCTCTGCTTTGCTTGGTTGTA 856
 806 TCGTGGACATAGCGCGTCACTCGTGGTTCCTAGGACCTTTTATTTATGTTGCGGATG 865
 857 CGGATTTAAACCCCGGTTCAATTAACAAATCTTACTTACTTAC---GGTAACCTAGGAA 912
 866 CGGGTTAAACCCCGGTTCAATTAACAAATCTTACTTACTTACGAGCGGTGCAACGGGAG 925
 913 ATTACTAGGCTCAATGAGCGCGGTTGGCAGAAC 946
 926 GGTATTATGCTCAATGAGCGGCTGTAGGCGGAAC 959

RESULT 5

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CG219364/c
LOCUS      CG219364      775 bp      DNA      linear      GSS 22-AUG-2003
DEFINITION OGWG30TV ZM 0.7-1.5 KB Zea mays genomic clone ZMMBMA0575F12,
            genomic survey sequence.
ACCESSION  CG219364
VERSION     CG219364.1 GI:34119252
KEYWORDS    GSS.
SOURCE      Zea mays
ORGANISM    Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1 (bases 1 to 775)
AUTHORS     Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
            Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
            Citek,R.W., Numborg,A., Robbins,D. and Lakey,N.
            Consortium for Maize Genomics
            Unpublished (2002)
            Other GSSs: OGWG30TH
            Contact: Cathy Whitelaw
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA
            Tel: 301-838-5843
            Fax: 301-838-0208
            Email: whitelaw@tigr.org
            Seq primer: TF
            Class: sheared ends.
            Location/Qualifiers
                1..775
                /organism="Zea mays"
                /mol_type="genomic DNA"
                /strain="B73"
                /db_xref="taxon:4577"
                /clone="ZMMBMA0575F12"
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                /note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb
                methylation filtered genomic DNA library"

ORIGIN
Query Match      28.5%; Score 485.4; DB 29; Length 775;
Best Local Similarity 77.5%; Pred. No. 4.9e-44;
Matches 601; Conservative 0; Mismatches 171; Indels 3; Gaps 1;

Y 221  CACCTACCTCCTCTTTTCGGCTACTCGTGTCTTTTCTATGAGCTCGGCTTCGGCATGCT 280
      |||
b 775  CAGTACCTGCTCTTCTCGGCTACTCGTGTCTGCCCATGAGCTCGGCTTCGGCATGCT 716
      |||
Y 281  CTGCGCGGCTCGTCCGCGCAAGAACACCATGAACATCATGCTCACCACGCTCTGGA 340
      |||
b 715  GTGCGCGGCTCGTCCGCGCAAGAACACCATGAACATCATGCTCACCACGCTCTGGA 656
      |||
Y 341  CGTTCGCGGGGGGCTCTTCTACTACTCTTCGGCTTCGGCTTCGGCTTCGGCTCCCC 400
      |||
b 655  CGCGCGCGGGGGGCGCTCTTCTACTACTCTTCGGCTTCGGCTTCGGCTTCGGCGAGCC 596
      |||
Y 401  CTCACACGGCTTCATCGTAAACATTTCTTCGGCTCAAGACATCCCTTCATCTCTCTA 460
      |||
b 595  CTCACACGGCTTCATCGGCAAGAGTTCTTCGGGTCAAGACCTGCCAGGACCGGCTT 536
      |||
Y 461  CGACTACAGCTACTTCTCTTACATAGGCGCTTCGCCATTCGCGCGCGCGGCATCACAG 520
      |||
b 535  CGACTACAGCTACTTCTCTTACATAGGCGCTTCGCCATTCGCGCGCGCGGCATCACAG 476
      |||
Y 521  CGGAAGCATCGCGGAAGCACAGTTCGTGGCCCTATCTCATCTACTCTCTCTCTCTCAC 580
      |||
b 475  GGCTCTCATCGCGAGGACCAAGTTGTGCTTACTCTATCTACTCTCGGGTTCCTGAC 416
      |||
Y 581  CGGCTTCGCTATCCGGTGGTCTCCACTGTTCTGTTGTTCCCGACAGCGCTGGGCTCTGC 640
      |||
b 415  GGGGTTTCGTTACCCCGTGGTGTGCACTGTTCTGTTGTTCCCGACAGCGCTGGGCGGCG 356
      |||
Y 641  CTTTAAGATCACCGACCGGCTATTTC---ACCGGCGTATAGACTTCGCGGTTCCGG 697
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Db 355  CAGCCGCCACGTCGCGCCCGCTGCTCTTCGCGGTCCGCGCTCATCGACTTCGCGGCTCGG 296
Qy 698  CGTAGTCCACATGTCGCGGAATAGCCGGCTATGGGAGCGCTGATCGAAGGCCCAAG 757
Db 295  CGTCGTCACATGTCGCGGCATCGCGGGCTGTGGGGCGCGCTCATCGAGGCCCCCG 236
Qy 758  AATGGACGTTTTCGATCATGACAGACGAGCTGTGGCCTTTCGAGGCCACACGCGGTCCTT 817
Db 235  CATCGGGCGCTTCGACCAACGCGCGCGCTCCGTCGCGCTCAAGGGCCACACGCGGTCGT 176
Qy 818  AGTAGTCCTGGGAACCTTCTTCTTTCGTTTGGTTGGTACGATTAAACCCGGTTCATT 877
Db 175  CGTGTGCTCGGCACCTTCTGCTGTGTTTCGCTGGTTCACCCCGGTCCTT 116
Qy 878  TAAACAAATCTTACTTACTTACGTAACCTACGAAATTTACTACGTTCAATGAGCGGGT 937
Db 115  CACCACCATCTTCAAGTCGTACGCGCCGCGCGGACCGTCCACGGGAGTGTGTCGGCGT 56
Qy 938  TGGCAGACCGGGTCACCACTACCTAGCGGGTCAACAGCTGCCTTGACCAG 992
Db 55  GGGCGCACCGCGCGTCACACACCCCTCGCGGAGCGTTCGCGGCTCACACG 1

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RESULT 6
LOCUS    CK290978
DEFINITION 941 bp mRNA linear EST 15-DEC-2003
            EST753692 Nicotiana benthamiana mixed tissue cDNA library,
            normalized, full-length Nicotiana benthamiana cDNA clone NEMB69 5',
            end, mRNA sequence.
ACCESSION  CK290978
VERSION     CK290978.1 GI:39870973
KEYWORDS    EST.
SOURCE      Nicotiana benthamiana
ORGANISM    Nicotiana benthamiana

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE   1 (bases 1 to 941)
AUTHORS     Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A., Day,B.,
            Staskiewicz,B., Jin,H. and Baker,B.
            Generation of EST sequences from Nicotiana benthamiana
            Unpublished (2003)
            Other ESTs: EST753693
            Contact: Robin Buell
            The Institute for Genomic Research
            9712 Medical Center Dr, Rockville, MD 20850, USA
            Email: potato-array@tigr.org
            Clones can be requested from TIGR via potato@tigr.org
            Seq primer: ATT TAG GTG ACA CTA TAG.
            Location/Qualifiers
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                /organism="Nicotiana benthamiana"
                /mol_type="mRNA"
                /db_xref="taxon:4100"
                /clone="NEMB69"
                /tissue_type="abiotic and biotic stress-treated leaves,
                callus tissue and root tissue"
                /lab_host="DH10B-Tona"
                /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                library, normalized, full-length"
                /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
                supplier: RNA was isolated from Nicotiana benthamiana
                tissues that include callus, roots from liquid culture
                grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                challenged leaves (Pseudomonas syringae pv tomato 12 hr;
                Xanthomonas campestris pv campestris 12 hr, 18hr;
                Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                campestris pv vesicatoria 18hr). RNA was isolated from
                these tissues and pooled in approximately equal molar
                amounts."

```

```

TITLE       The Institute for Genomic Research
JOURNAL     9712 Medical Center Dr, Rockville, MD 20850, USA
COMMENT     Email: potato-array@tigr.org
            Clones can be requested from TIGR via potato@tigr.org
            Seq primer: ATT TAG GTG ACA CTA TAG.
            Location/Qualifiers
                1..941
                /organism="Nicotiana benthamiana"
                /mol_type="mRNA"
                /db_xref="taxon:4100"
                /clone="NEMB69"
                /tissue_type="abiotic and biotic stress-treated leaves,
                callus tissue and root tissue"
                /lab_host="DH10B-Tona"
                /clone_lib="Nicotiana benthamiana mixed tissue cDNA
                library, normalized, full-length"
                /note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
                supplier: RNA was isolated from Nicotiana benthamiana
                tissues that include callus, roots from liquid culture
                grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
                cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
                challenged leaves (Pseudomonas syringae pv tomato 12 hr;
                Xanthomonas campestris pv campestris 12 hr, 18hr;
                Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
                campestris pv vesicatoria 18hr). RNA was isolated from
                these tissues and pooled in approximately equal molar
                amounts."

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FEATURES
source

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ORIGIN

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RESULT 7
 FK282541
 LOCUS CK282541 968 bp mRNA linear EST 15-DEC-2003
 DEFINITION EST745263 Nicotiana benthamiana mixed tissue cDNA library,

Db 823 CCGGGTTCCTTTAATAAGATTCTAGTTACCTATGGTACAAAGTGGAGGGTATTATGGTCAA 882

QY 927 TGGAGCGGGTGGCAGAAACCGGGTACACCTACCTAGCGG 969

Db 883 TGGAGTCTGTGGGACGTACCGGGTGACCAACCTTAGCGG 925

RESULT 9

CK289847

LOCUS

DEFINITION

EST752569 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMBQ69 5',
end, mRNA sequence.

ACCESSION

CK289847

VERSION

CK289847.1 GI:39868739

SOURCE

ORGANISM

Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE

1 (bases 1 to 970)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.

AUTHORS

Staskawicz, B., Jin, H. and Baker, B.

TITLE

Generation of EST sequences from Nicotiana benthamiana

JOURNAL

Unpublished (2003)

COMMENT

Other ESTs: EST752570

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GGG ACA CTA TAG.

Location/Qualifiers

1. 970

/organism="Nicotiana benthamiana"

/mol_type="mRNA"

/db_xref="taxon:4100"

/clone="NEMBQ69"

/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"

/lab_host="DH10B-TonA"

/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"

/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Query Match 27.8%; Score 474; DB 14; Length 970;
Best Local Similarity 72.2%; Pred. No. 7.7e-43;
Matches 631; Conservative 0; Mismatches 240; Indels 3; Gaps 1;

Y 87 GCTTGTCCCGCCGAGCAACTGGCCCACTTCTGCGCCCAACACACAGAGCGCTCCGCC 146

b 100 GCTTGTGAAGTAGAACCAACTGGCTCCATCTCTCGGACCCCAACACCGCGGTAGCC 159

Y 147 GCGCGCTCCCTTATCTGCGGGCCATTTGCGCGCGTGGACAGCAAGTTCGTCGACCGGCC 206

b 160 GCTGCGCACTTATCTGTTAGCAACATCTCCGATGTCTCAACAGATTTATTGATACCGGC 219

Y 207 TTGCGCGTCGACAAACACTACTCTCTCTTTTCCGCGCTACCTCGTTTCTATGCAAGCTC 266

b 220 TAGCGTATCGACTCGACTTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 279

QY 267 GGCTTCGCGCATCTCTGCGCGGCTCCGTCCGCGCAAGAACACCATGAAACATCATGCTC 326

Db 280 GGCTTCGCTATGCTTTGTGCGGGCTCTGTCCGTGCGAAATAACAATGATGCTT 339

QY 327 ACCAAGCTCTCGAGCGCTGCGCGCGGCGCTCTCTACTACTCTCTCTCGGCTTGGCCTTC 386

Db 340 ACTAATGTTCTTGACGCTGCGCTGCTGGGATTTTCTACTATCTTTTGGCTTCGCTTC 399

QY 387 GCTTTCGCGTCCCTCCCAAGGTTTCATCGGTAAACAATTTCTTCGCGCTCAAGGACATC 446

Db 400 GCTTGGGCGGGCGGCTTAAACGGCTTCATTCGGGCTCACTTCTTTGGCTTAAAGAGATC 459

QY 447 CTTTCATCTCTCTAGAGCTACAGACTTCTCTCTACCAATGGGCTTCGCCATCGCGGCC 506

Db 460 CTTCTACTCTCTTTGATTACAGTAATTTCTGTACCAATGGGCAATTTGCTATAGCGGCC 519

QY 507 GCGGCGATCACAGCGGAAGCATCCCGAAGCAGACACACAGTTTCGTGGCTATCTCATCTAC 566

Db 520 GCTGGAATTTACTAGCGGCTCTATAGCCGAGAGGACTCAGTTTGTGCTTATTGATTTAC 579

QY 567 TCCTCTCTCTCTCACCGGCTTCGTCTATCCGGTGTCTCCCACTGGTTCTGGTCCCGAGAC 626

Db 580 TCTTCTTTTCTTACCGGCTTTGTTTACCGGTTGTTTCTCATTCATTCGTTTGGTCCCGAG 639

QY 627 GCGTGGCGCTCTGCTCTTTAAGATCACCGACCGGCTATTTTCCACCGCGCTAAATAGATTTC 686

Db 640 GGTGGGCGC---AGCCCGACCAATTTCAAATTTGTTTTCGGGTCGGGTATTCGACTTT 696

QY 687 GCGGTTTCGGGCTAGTCCACATGTCGGCGGAATAGCCGCTATGGGAGCGCTGATC 746

Db 697 GCTGGGTCCGGTGTAGTTTCATATGTTAGGTGGTATAGCCGGGTTTATGTTGCTTTAAT 756

QY 747 GAAGGCCCAAGAAATGGGACGTTTCGATCATCAGAGAGAGCTGTGGGCTTCGAGAGGCCAC 806

Db 757 GAAGTTCACAAATCGGACGTTTCGATCATCAGGCTCGGTCGGTCCGTTCCGTTGGGCTAT 816

QY 807 ACGGCTCTCTAGTACTCTCGGAAACCTTCTTCTGTTTGGTTCGTTTCGTTACGATTTAAC 866

Db 817 ACGGCTCTCTGTTGGTTTTCGGTACCTTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 876

QY 867 CCGGTTTCATTTAAACAAATCTACTTACTTACCGTAACCTCAGGAAATTTACTACGGTCAA 926

Db 877 CCGGTTCTTTTATAAGATCTTAGTTACCTATGTCACAGTGGAGGGTATTATGGTCAA 936

QY 927 TGGAGCGGGTGGCAGAACCGCGGTGACCACTA 960

Db 937 TGGAGTGTGTGGGACGTACCGCGGTGACCACTA 970

RESULT 10

CK287788

LOCUS

DEFINITION

EST750510 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMB81 5',
end, mRNA sequence.

ACCESSION

CK287788

VERSION

CK287788.1 GI:39864664

KEYWORDS

EST

SOURCE

ORGANISM

Nicotiana benthamiana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.

REFERENCE

1 (bases 1 to 971)

Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.

AUTHORS

Staskawicz, B., Jin, H. and Baker, B.

TITLE

Generation of EST sequences from Nicotiana benthamiana

JOURNAL

Unpublished (2003)

COMMENT

Other ESTs: EST750511

Contact: Robin Buell

The Institute for Genomic Research

9712 Medical Center Dr, Rockville, MD 20850, USA

Email: potato-array@tigr.org

Clones can be requested from TIGR via potato@tigr.org

Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES

source

1..971
/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NEMBB81"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

Query Match 27.1%; Score 463; DB 14; Length 971;
Best Local Similarity 72.2%; Pred. No. 1.2e-41;
Matches 631; Conservative 0; Mismatches 240; Indels 4; Gaps 2;

QY 87 GCTTGTCCCGCGAACAACCTGCGCCCAACTTCGCGCCCAACACACAGAGCTCCGCC 146
DB 100 GCTTGTGAAGTAACCAACTGGCTCCACTTCCTCGGACCAACACACAGCGGTAGCC 159
QY 147 GCGGCTCCCTTATCTGGCGGCAATTCGCCCGCTGGACAGCAAGTTCGFCGACAGGCC 206
DB 160 GCTGCCACTTATCTGTAGCCAACTTCCTCGATGTGTCGACAGTTTATTGATACGGC 219
QY 207 TTGCGCGTCGACACACCTACTCTCTTTTCGCGCTACCTCGTTTTCCTATGAGCTC 266
DB 220 TAGCGTATCGACTGACTTATCTCTCTCTCTCGCTTACCTTGTCTTTTCATCGAGCTC 279
QY 267 GCGTTCGCTATGCTCTGGCGGCTCGCTCGCGCCCAAGAACACCATGACATCATGCTC 326
DB 280 GCGTTCGCTATGCTTGTGGGCTCTGCTGGGAAATACATGACATATGCTT 339
QY 327 ACCAAGTCTCGAGCTGCGCGCGCTCTTCTACTACCTCTTCGCTTCGCTTC 386
DB 340 ACTAATGTTCTTGACGCTCGCGCTGGTGGATTTTCTACTATCTTTTGGCTTCGCTTC 399
QY 387 GCTTTCGCTCCCTCCCAACGGCTTCATCGGTAAACATTTCTTCGCGCTCAAGGACATC 446
DB 400 GCTTGGCGGGCGCTTAACCGGCTTCAATGGGCTCACTTCTTGGGCTTAAGGAGATC 459
QY 447 CTTTCACTCTCTAGACTACAGTACTTCTCTACGATGGGCTTCGCGCTTCGCGCGCC 506
DB 460 CTTTCACTCTCTTGTGATACAGTAAATTTCTGTACCAATGGGCAATTTGTATAGCGCC 519
QY 507 GCGGATCACACAGCGGAGACATCGCGAACGACACAGTTCGTTGGCTATCTCATCTAC 566
DB 520 GCTGGAATTAATAGCGGCTCTATAGCGAGGAGTCACTTGTCTGCTTATTTGATTTAC 579
QY 567 TCTCTCTCTCTACCGGCTTCTATCGGTGTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 626
DB 580 TCTCTCTCTCTACCGGCTTCTTATACCGGCTTCTATCGGTGTCTGCTGCTGCTGCTGCTGCT 639
QY 627 GCGTGGGCTCTGCTTAAAGTACACCGCGCTATTTTCCACCGCGCTAATAGACTTC 686
DB 640 GGGTGGGCTCTGCTTAAAGTACACCGCGCTATTTTCCACCGCGCTAATAGACTTC 696
QY 687 GCGGTTTCGCGGTATGTCACATGTCGCGGATATAGCGGCTCTATCGGAGCGCTGATC 746
DB 697 GCTGGGTGCGGTGTATGTTATATAGTAGGTGTATAGCGGCTTATGTTGTTTAAAT 756

ORIGIN

Query Match 27.1%; Score 463; DB 14; Length 971;
Best Local Similarity 72.2%; Pred. No. 1.2e-41;
Matches 631; Conservative 0; Mismatches 240; Indels 4; Gaps 2;

QY 87 GCTTGTCCCGCGAACAACCTGCGCCCAACTTCGCGCCCAACACACAGAGCTCCGCC 146
DB 100 GCTTGTGAAGTAACCAACTGGCTCCACTTCCTCGGACCAACACACAGCGGTAGCC 159
QY 147 GCGGCTCCCTTATCTGGCGGCAATTCGCCCGCTGGACAGCAAGTTCGFCGACAGGCC 206
DB 160 GCTGCCACTTATCTGTAGCCAACTTCCTCGATGTGTCGACAGTTTATTGATACGGC 219
QY 207 TTGCGCGTCGACACACCTACTCTCTTTTCGCGCTACCTCGTTTTCCTATGAGCTC 266
DB 220 TAGCGTATCGACTGACTTATCTCTCTCTCTCGCTTACCTTGTCTTTTCATCGAGCTC 279
QY 267 GCGTTCGCTATGCTCTGGCGGCTCGCTCGCGCCCAAGAACACCATGACATCATGCTC 326
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QY 327 ACCAAGTCTCGAGCTGCGCGCGCTCTTCTACTACCTCTTCGCTTCGCTTC 386
DB 340 ACTAATGTTCTTGACGCTCGCGCTGGTGGATTTTCTACTATCTTTTGGCTTCGCTTC 399
QY 387 GCTTTCGCTCCCTCCCAACGGCTTCATCGGTAAACATTTCTTCGCGCTCAAGGACATC 446
DB 400 GCTTGGCGGGCGCTTAACCGGCTTCAATGGGCTCACTTCTTGGGCTTAAGGAGATC 459
QY 447 CTTTCACTCTCTAGACTACAGTACTTCTCTACGATGGGCTTCGCGCTTCGCGCGCC 506
DB 460 CTTTCACTCTCTTGTGATACAGTAAATTTCTGTACCAATGGGCAATTTGTATAGCGCC 519
QY 507 GCGGATCACACAGCGGAGACATCGCGAACGACACAGTTCGTTGGCTATCTCATCTAC 566
DB 520 GCTGGAATTAATAGCGGCTCTATAGCGAGGAGTCACTTGTCTGCTTATTTGATTTAC 579
QY 567 TCTCTCTCTCTACCGGCTTCTATCGGTGTCTCCGCTGCTGCTGCTGCTGCTGCTGCTGCT 626
DB 580 TCTCTCTCTCTACCGGCTTCTTATACCGGCTTCTATCGGTGTCTGCTGCTGCTGCTGCTGCT 639
QY 627 GCGTGGGCTCTGCTTAAAGTACACCGCGCTATTTTCCACCGCGCTAATAGACTTC 686
DB 640 GGGTGGGCTCTGCTTAAAGTACACCGCGCTATTTTCCACCGCGCTAATAGACTTC 696
QY 687 GCGGTTTCGCGGTATGTCACATGTCGCGGATATAGCGGCTCTATCGGAGCGCTGATC 746
DB 697 GCTGGGTGCGGTGTATGTTATATAGTAGGTGTATAGCGGCTTATGTTGTTTAAAT 756

QY 747 GAAGGCCCAAGATGGAGCTTTCGATCATCGACGAGCTGTGGCTTCGAGGCCAC 806
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QY 807 AGGCGCTCTTATAGTCTCTGGGAACTTCTTGTGTTTGGTTCGTTAGGATTAAC 866
DB 817 AGGCGCTCTTATAGTCTCTGGTTCGTTTGTGTTTGGTTCGTTAGGATTAAC 876
QY 867 CC-CGGTTCATTTAAACAATCTTACTTACGTTAACTCAGAAATTAACAGGTCA 925
DB 877 CCGGCTCTCTTATAGATCTTACCTATGTTACAGTGGAGGTATATGTTCA 936
QY 926 ATGAGCGCGGTTCGAGAAACCGCGTCAACCTA 960
DB 937 ATGAGTGTCTGGGACGTACCGGTTGACCA 971

RESULT 11
CK294612 975 bp mRNA linear EST 15-DEC-2003
LOCUS ESR757326 Nicotiana benthamiana mixed tissue cDNA library,
DEFINITION normalized, full-length Nicotiana benthamiana cDNA clone NEMCO68 5'
end, mRNA sequence.
CK294612
CK294612.1 GI:39878176
EST.
SOURCE Nicotiana benthamiana
ORGANISM Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
REFERENCE 1 (bases 1 to 975)
AUTHORS Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
TITLE Generation of EST sequences from Nicotiana benthamiana
JOURNAL Unpublished (2003)
COMMENT Other ESTs: ESR757327
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.

FEATURES
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1..975
/organism="Nicotiana benthamiana"
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/clone="NEMCO68"
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callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN
Query Match 27.0%; Score 460.2; DB 14; Length 975;
Best Local Similarity 72.2%; Pred. No. 2.4e-41;
Matches 627; Conservative 0; Mismatches 238; Indels 4; Gaps 2;
QY 87 GCTTGTCCCGCGAACAACCTGCGCCCAACTTCGCGCCCAACACACAGAGCTCCGCC 146

111 GCTTGTGAAGTGAACCACTGGCTCCATTCCTCGGACCCAAACACCAACGCGCGTAGCC 170
147 GCGCGCTCCCTTATCTGCGGCCATTTGCGCGCGGTGGAGCAAGTTCGTGGACACGCGCC 206
171 GCTGCCACTTATATCTGTAGCAATCTCCGATGTGTCCAAACAGTTATTGTATACGCGC 230
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231 TAGCTATGACCTGACCTATCTCCCTTCCTCGGTACCTTGTGTTTTCATGAGCTC 290
267 GGTTCGCCATGCTCTGCGCGGCTCCGTCGCGCGCAAGAACACCAACATCATGCTC 326
291 GGTTCGCTATGCTTTGTGCGGCTCTGTCCGTCGCGAAATACAAATGAACTATGCTT 350
327 ACCAAGCTCTGAGCGCTGCGCGCGGCGCTCTTCTACTACCTTCCTCGGCTTCGCTTC 386
351 ACTAATGTTCTTGACGCTGCGGTGTGTGGATTTTCTATCTATCTTTTGGCTTCGCTTC 410
387 GCTTTCGGCTCCCTCCCAACGCTTCATCGGTAAACATTTCTCGGCTCAAGGACATC 446
411 GCTTGGCGGGCGGCTTAACGCTTCATTGGCGCTCACTTCTTTGGCTTAAGGAGATC 470
447 CTTTCATCTCTACACCTACGACTACTTCTCTACCAATGGGCTTCGCCATCGCGCC 506
471 CTTTCTACTTCTTTTGAATACAGTAATTTCTGTACCAATGGGCAATTTGCTATAGCGCC 530
507 GCGCGCATCACCAGCGGAAGCATCGCGCAACGACACAGATTCGTGGCTATCTCATCTAC 566
531 GCTGGAATTACTAGCGCTCTATAGCGGAGAGACTCAGTTGTGCTTATTTGATTTAC 590
567 TCTCTCTCTCACCAGCTGCTATCGCGGTGCTCCCACTGGTTCTGTGTCGCCAGAC 626
591 TCTTCTTTTCTTACCGGCTTGTGTACCGGTTGTCTCATTTGTTTGTGTCGCCAGAT 650
627 GGTGGGCTCTGCTTTAAGATCACCGCGGCTATTTTCCACCGGCTAATAGACTTC 686
651 GGTGGGCT---AGCCCGACCAATCAATTTGTTATTCGGGTCGGGTGTTATGACTTT 707
687 GCGGTTTCGGGTAGTGCATATGTCGCGGAATAGCGGCTATGGGAGCGCTGATC 746
708 GCTGGTTCGGGTGTAGTTCATATGTTAGTGTGTATAGCGGCTTTATGTTGCTTAAT 767
747 GAAGGCCCAAGATGAGGCTTTTCATATGATGAGGAGGCTGTGGCTTCGAGGCGAC 806
768 GAAGGTCGAAGATCGAGGCTTCATATGCGGCTCGGTCGTTGCTCCGTGGGAT 827
807 AGCGCTCTTATGCTCTCGGAACTCTTCTGTTGCTTGGTTGCTGAGGATTTAAC 866
828 AGCGCTTCGCTTGTGTTTGGTACCTTTTGTGTTGCTTGGTTGCTGAGGTTAAC 887
867 CCGGCTTCATTTAACAATCTCTACTTACTAGGTAAGTACAGGAAATACAGGTCAC 926
888 CCGGCTC-TTTAATAGATTTAGTTACTATGTTAGTACAGTGGAGGTATTATGGTCAA 946
927 TGGAGCGCGTTTGGCAGAACCGGCTCAC 955
947 TGGAGTGTGTGGAGCTACCGGCTGAC 975

RESULT 12
LOCUS CK285989 961 bp mRNA linear EST 15-DEC-2003
DEFINITION EST748711 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NEMAY92 5'
end, mRNA sequence.
CK285989
CK285989.1 GI:39861109
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 961)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskawicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Unpublished (2003)
Other ESTs: EST748712
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers

FEATURES
source

1..961
/organism="Nicotiana benthamiana"
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/db_xref="taxon:4100"
/clone="NEMAY92"
/tissue type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomato 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

ORIGIN

Query Match 26.6%; Score 453.8; DB 14; Length 961;
Best Local Similarity 71.7%; Pred. No. 1.2e-40;
Matches 623; Conservative 0; Mismatches 242; Indels 4; Gaps 2;
QY 87 GCTTGTCCGCGGCAACACTGGCCCACTTCTCGGCCAAACACCAACGCGCTCCGCC 146
DB 97 GCTTGTGAAGTGAACCACTGGCTCCATTCCTCGGACCCAAACACCGCGGTAGCC 156
QY 147 GCGGCTCCCTTATCTGCGGCAATTCGCGCGGTGGAGCAAGTTCGTGACACGCGC 206
DB 157 GCTGCCACTTATATCTGTAGCAATTCCTCGATGTGTCCAAAGTTTATGATACGCGC 216
QY 207 TTGCGCGTGGACAAACCTACCTCTCTTTTTCGCGCTACCTCGTTTTCATGAGCTC 266
DB 217 TAGCTATGAGCTGACCTATCTCTCTCTTCTCGGCTTACCTGTTTTCATGAGCTC 276
QY 267 GCTTTCGCGCTCTGCGCGGCTCCGTCGCGCCCAAGAACACCAACATCATGCTC 326
DB 277 GCTTTCGCTATGCTTTGTGCGGCTCTGTCCGTGCGAAATACAAATGAACTATGCTT 336
QY 327 ACCAAGCTCTGAGCGCTGCGCGGCGGCTCTTCTACTACCTCTTCGCTTCGCGCTC 386
DB 337 ACTAATGTTCTTGACGCTGCGGCTGGTGGGATTTTCTATCTCTTTTGGCTTCGCTTC 396
QY 387 GCTTTCGCGCTCCCTCCAAACGCGCTTCATCGGTAAACATTTCTTCGCGCTCAAGGACATC 446
DB 397 GCTTGGGCGGGCGGCTCTAACCGCTTCATTGGGCGTCACCTTCTTTGGCTTAAGGAGATC 456
QY 447 CTTTCATCTCTTACGACTACGACTACTTCTCTACCAATGGGCTTCGCCATCGCGCC 506
DB 457 CTTTCTACTTCTTTTGAATACAGTAATTTTCTGTACCAATGGGCAATTTGCTATAGCGCC 516
QY 507 GCGGCGATCACAGCGGAAGCATCGCGCAACGACACAGATTCGTGGGCTATCTCATCTAC 566
DB 517 GCTGGAATTACTAGCGGCTCTATAGCGGAGGACTCAGTTTCTGCTTATTTGATTTAC 576

JOURNAL
COMMENT

Unpublished (2000)
Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M272814e TIGR sequence name:
MTKAU93TK More information is available at:
http://chrysis.tamu.edu/medicago
Seq primer: SKmod (CTA GAA GTg gAT CC).
Location/Qualifiers
1. .847

FEATURES
source

/organism="Medicago truncatula"
/mol_type="mRNA"
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/clone="PGVSN-13017"
/tissue_type="senescent root nodules"
/dev_stage="mixture of effective nodules from 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage"
/lab_host="E. coli strain SOLR"
/clone_lib="GVSN"
/note="Vector: pBluescript SK +/-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA from the mixture of effective nodules of 40 day old plants harvested 36 hours post shoot removal and nodules collected from 2 month old plants at mid-pod stage. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in SOLR cells."

RIGIN

Query Match 26.0%; Score 443.2; DB 10; Length 847;
Best Local Similarity 70.5%; Pred. No. 1.9e-39;
Matches 592; Conservative 0; Mismatches 248; Indels 0; Gaps 0;

42 TCAGTCACGGCTAATACACTAACCAACCCACCATGTCGCTGCTGTCGCGCGGAA 101
47 TAAGCAGCTTCGTCACCACTACCCACCAACATGTCGTCGCGGAATGTCAGTTTCG 66
102 CAACTGCGCCAACTTCTCGGCGCAACACCAACAGCGCTCGCGCGGCTCCCTTATC 161
67 CAGTAGCACAGTTTCATCGGCGCCCAACGCCACCAACGCCGCGGCAATTTTCATC 126
162 TGGGCGCATTCGCGCGCGTGAAGAGAGAGTTCGTCGACAGCGGCTTCGCGTCGACAC 221
127 TGGGACCACTTGACAGCAGTGTCAACACAGATTCGTTGACACACAATTCGCTGTGACAC 186
222 ACCTACTCTCTCTTTTCGCGCTTACCTCGTTTTTCTATGAGCTCGGCTTCGCGCATGCTC 281
187 ACCTATCTTTTATCTCAGCTTACCTGCTCTCTATGCACTGTTTTCGCAATGCTC 246
282 TGGCGCGCTTCGTCGCGCGCAAGAACACCATGAAATCATGCTCACAACAGCTCTGGAC 341
247 TGTGCTGGTTCAGTTTCGTCGTAAGAACCAACATCATCATCTCACAATGTTCTCGAC 306
342 GTTCGCGCGCGGCGCTCTTCTACTTACTCTTCTCGCTTCGCTTCGCTTCGCTCGCC 401
307 GCGCTGCTGGCGGTGTTTCTACTATCTCTTCGTTTTCGCTTCGCAACACT 366
402 TCCACGGCTTCATCGGTAAACATTTCTCGGCTTCAGGACATCCCTTCATCTCTCTAC 461
367 TCAATAGTTTTCATAGGAAAACATTTCTCGCTCTGAAGATGTTCCGACAGCAATTTT 426
462 GACTACAGCTACTTCTCTTACCAATGGGCTTCGCAATCGCGCGCGGCGCATCACAGC 521
427 GATTACAGTTATTTCTTTATCAATGGGCTTTGCTATAGACCGCTGTTATCACAGC 486

QY 522 GGAGCATCGCGGAACGACACACAGTTCGTGGCCCTATCTCATCTACTCTCTCTCACC 581
DB 487 GGCCTATAGCGGAACGAACCTCAGTTGCTGCTTATCTATATACTCACTTTCTCACA 546
QY 582 GCTTCGCTATACCGGTGCTCCACTGTTCTGTCGTCGCGGCTGGGCTCTGTC 641
DB 547 GGGTTTGTATTACCCCTGTGGTTCTCATTTGGTCTGCGGTGATGTTGGGCTAGCGCA 606
QY 642 TTTAAGATACACCGCGCTATTTTCCACCGGCTAATAGACTTCGCGGTTCCGCGCTA 701
DB 607 ACCAACCGGCAACCTACTCTTTGGTACAGAGTCAATGATTTTCTGCTCGGCTGTT 666
QY 702 GTCCACATGCTCGCGGAATAGCGGCTATGCGGAGCGCTGATGCAAGGCCCAAGATG 761
DB 667 GTTCATATGTTGGTGTGTTATTTGCTGCTTTTGGGAGCACTCATTTGAAGGTCACGAA 726
QY 762 GGAGCTTTTCGATCATGACGAGCAGCTGTGCGCTTCGAGGCGCACAGCGCTTAGTA 821
DB 727 GACCGTTTCGATCACTCTGTCGAGCGGTAGCTCTTCGCGGACACAGTGTCTTCTGTT 786
QY 822 GTCTCGGAACCTTTCTGCTTTGCTTGGTTGCTGCTGATGCGGATTTAACCCCGGTTCA 881
DB 787 GTTCTTGTACCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 846

RESULT 15
CK280628 984 bp mRNA linear EST 15-DSG-2003
EST743350 Nicotiana benthamiana mixed tissue cDNA library,
normalized, full-length Nicotiana benthamiana cDNA clone NBMA146 5',
end, mRNA sequence.
CK280628
CK280628.1 GI:39850448
EST.
Nicotiana benthamiana
Nicotiana benthamiana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Nicotiana.
1 (bases 1 to 984)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A., Day, B.,
Staskiewicz, B., Jin, H. and Baker, B.
Generation of EST sequences from Nicotiana benthamiana
Other ESTs: EST743349 EST743351 EST743352
Unpublished (2003)
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: ATT TAG GTG ACA CTA TAG.
Location/Qualifiers
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/organism="Nicotiana benthamiana"
/mol_type="mRNA"
/db_xref="taxon:4100"
/clone="NBMA146"
/tissue_type="abiotic and biotic stress-treated leaves,
callus tissue and root tissue"
/lab_host="DH10B-Tona"
/clone_lib="Nicotiana benthamiana mixed tissue cDNA
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/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomatos 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

FEATURES
source

/organism="Nicotiana benthamiana"
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callus tissue and root tissue"
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library, normalized, full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Nicotiana benthamiana
tissues that include callus, roots from liquid culture
grown plants, heat-stressed leaves (38 C, 3 hr and 6 hr),
cold-stressed leaves (5 C 3 hr, 6hr), and pathogen
challenged leaves (Pseudomonas syringae pv tomatos 12 hr;
Xanthomonas campestris pv campestris 12 hr, 18hr;
Pseudomonas syringae pv phaseolicola 18hr, and Xanthomonas
campestris pv vesicatoria 18hr). RNA was isolated from
these tissues and pooled in approximately equal molar
amounts."

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:52:48 ; Search time 60 Seconds
(without alignments)
2354.563 Million cell updates/sec

Title: US-10-033-109-4

Perfect score: 2639

Sequence: 1 MSLPACPAEQLAQLGPNNTT.....HGMLRRVGNASSTPTTDE 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_29Jan04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1980s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Match	Length	DB ID	Description
1	2639	100.0	500	6	AAO26533 Soybean h
2	2129.5	80.7	501	2	AAR74676 Arabidops
3	2129.5	80.7	501	3	AAG40620 Arabidops
4	2129.5	80.7	510	3	AG36233 Arabidops
5	1954	74.0	494	6	AAO26534 Arabidops
6	1943	73.6	446	3	AAO40821 Arabidops
7	1943	73.6	455	3	AAO40821 Arabidops
8	1943	72.5	440	3	AAO40622 Arabidops
9	1913	72.5	449	3	AAO40622 Arabidops
10	655.5	24.8	651	4	AB362422 Arabidops
11	613	23.2	183	6	AAO26532 Arabidops
12	491	18.6	401	5	AB362422 Arabidops
13	488	18.2	431	5	AB362422 Arabidops
14	481.5	18.2	431	5	AB362422 Arabidops
15	452.5	17.1	413	5	AB362422 Arabidops
16	441	16.7	431	5	AB362422 Arabidops
17	430.5	16.3	438	4	AAO26533 Arabidops
18	428	16.2	428	6	ABM70704 Arabidops
19	406.5	15.4	437	5	AB362422 Arabidops
20	403.5	15.3	488	6	AB362422 Arabidops
21	400	15.2	428	6	AB362422 Arabidops
22	400	15.2	428	6	AB362422 Arabidops
23	366	13.9	475	5	AB362422 Arabidops
24	363.5	13.8	452	4	AB362422 Arabidops
25	363.5	13.8	452	4	AB362422 Arabidops

26	335.5	12.7	470	6	AAO26538 Wheat hig
27	327.5	12.4	486	6	AAO26537 Soybean h
28	314	11.9	497	6	AAO26536 Rice high
29	301	11.4	924	4	AB362085 Novel hum
30	204.5	7.7	339	5	AB362085 Novel hum
31	204.5	7.7	347	5	AB362085 Novel hum
32	202.5	7.7	347	5	AB362085 Novel hum
33	193	7.3	223	7	AB362085 Novel hum
34	182	6.9	224	7	AB362085 Novel hum
35	173.5	6.6	441	5	AB362085 Novel hum
36	173.5	6.6	441	5	AB362085 Novel hum
37	152	5.8	449	4	AB362085 Novel hum
38	151	5.7	498	5	AB362085 Novel hum
39	148	5.6	455	5	AB362085 Novel hum
40	139	5.3	473	3	AB362085 Novel hum
41	139	5.3	479	3	AB362085 Novel hum
42	139	5.3	479	3	AB362085 Novel hum
43	139	5.3	479	3	AB362085 Novel hum
44	139	5.3	479	3	AB362085 Novel hum
45	137	5.2	443	6	AB362085 Novel hum

ALIGNMENTS

RESULT 1
AAO26533
ID AAO26533 standard; protein; 500 AA.
AC AAO26533;
XX
XX
DT 18-FEB-2003 (first entry)
XX
DE Soybean high affinity ammonium transporter protein.
XX
KW Herbicide; ammonium transporter protein; herbicide; transgenic plant;
KW soybean.
XX
OS Glycine max.
XX
PN US2002142390-A1.
XX
PD 03-OCT-2002.
XX
PF 28-DEC-2001; 2001US-00033109.
XX
PR 28-AUG-1998; 98US-0098248P.
PR 27-AUG-1999; 99US-00384625.
XX
XX (ALILE/) ALLEN S M.
XX (RAFA/) RAFALSKI J A.
XX
PI Allen SM, Rafalski JA;
XX
XX WPI; 2003-102520/09.
XX N-PSDB; AAL53985.
XX
PT Novel ammonium transporter polypeptide useful for identifying enzymatic
PT inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
PT transporter polypeptides.
XX
XX Claim 14; Page 14-16; 27pp; English.
XX
XX The invention relates to a novel ammonium transporter protein comprising
XX 90% homology based on the Clustal method compared to: a corn ammonium
XX transporter polypeptide of 183 or 63 amino acids; a soybean ammonium
XX transporter polypeptide of 500 or 486 amino acids; a wheat ammonium
XX transporter polypeptide of 494 or 470 amino acids; and a rice ammonium
XX transporter 497 amino acids fully defined in the specification. The
XX isolated polynucleotide is useful for selecting an isolated
XX polynucleotide that affects the level of expression of the ammonium
XX transporter polypeptide in a plant cell. The ammonium transporter protein
XX is useful for preparing antibodies which are useful for detecting the

CC transporter protein in situ in cells or in vitro in cell extracts, and as
 CC targets to facilitate design and/or identify inhibitors of the enzymes
 CC that are useful as herbicides. The isolated polynucleotide is also useful
 CC for creating transgenic plants in which the polynucleotide is present at
 CC higher or lower levels than normal, and for designing and producing
 CC primer pairs which are useful in amplification or primer extension
 CC reactions. This sequence represents the soybean high affinity ammonium
 CC transporter protein of the invention
 XX
 XX Sequence 500 AA;

Query Match 100.0%; Score 2639; DB 6; Length 500;
 Best Local Similarity 100.0%; Pred. No. 2.9e-252;
 Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSLPACPAEQLAQLLGNPTDASAAASLTCGHFAAVDSKFDVTAFAVDNTYLLFSAYLVF 60
 DB 1 MSLPACPAEQLAQLLGNPTDASAAASLTCGHFAAVDSKFDVTAFAVDNTYLLFSAYLVF 60
 2Y 61 SMQLGFAMLCAGSVRAKNTNMIMLTNVLDAAGLFFYLFGFAFAFGSPSNGFIKHF 120
 DB 61 SMQLGFAMLCAGSVRAKNTNMIMLTNVLDAAGLFFYLFGFAFAFGSPSNGFIKHF 120
 2Y 121 LKDIPTSSSYDYSLYQWAFIAAAGITSGSIAERTQFVAYLIYSSFLTGFFYPVSHWF 180
 DB 121 LKDIPTSSSYDYSLYQWAFIAAAGITSGSIAERTQFVAYLIYSSFLTGFFYPVSHWF 180
 2Y 181 WSPDGNWAFKITDRLFSTGVIDFAGSGVVMVGGIAGLWGLALIEGRPMGRFDHAGRAVA 240
 DB 181 WSPDGNWAFKITDRLFSTGVIDFAGSGVVMVGGIAGLWGLALIEGRPMGRFDHAGRAVA 240
 2Y 241 LRHGSASLVLTGFLWFGYGNFPGSFNKILLTYGNSGNYGQWSAVGRTAVTTLAGS 300
 DB 241 LRHGSASLVLTGFLWFGYGNFPGSFNKILLTYGNSGNYGQWSAVGRTAVTTLAGS 300
 2Y 301 TAALTTLFGKRVISGHNWNTDVCNGLLGGFAAITAGCSVVEPWAIVCGFVASIVLIACN 360
 DB 301 TAALTTLFGKRVISGHNWNTDVCNGLLGGFAAITAGCSVVEPWAIVCGFVASIVLIACN 360
 2Y 361 KLAEKVFDDEPLEAAQLHGGCGTGWVIFTALFAKKEVYKVEVYGLGRAHGLLWGGGKLLA 420
 DB 361 KLAEKVFDDEPLEAAQLHGGCGTGWVIFTALFAKKEVYKVEVYGLGRAHGLLWGGGKLLA 420
 2Y 421 ARVIQILVIAGWSATMGPLFWGLNKLKLLRISSEDELAGMDMTRHGGFAVAYEDETHK 480
 DB 421 ARVIQILVIAGWSATMGPLFWGLNKLKLLRISSEDELAGMDMTRHGGFAVAYEDETHK 480
 2Y 481 HGMQLRRVGNASSTPTTDE 500
 DB 481 HGMQLRRVGNASSTPTTDE 500

RESULT 2

BAR74676

ID AAR74676 standard; protein; 501 AA.

KX

AC AAR74676;

KX

DT 05-JAN-1996 (first entry)

KX

DE Arabidopsis thaliana ammonium transporter.

KX

KW Nitrogen metabolism; transgenic plant; ammonium transporter gene;

KX

KW antisense; inhibition; low input crop management.

KX

DS Arabidopsis thaliana.

KX

PN DE4337597-A1.

KX

PD 04-MAY-1995.

KX

CF 28-OCT-1993; 93DE-04337597.

KX

PR 28-OCT-1993; 93DE-04337597.
 XX (GENB-) INST GENBIOLOGISCHE FORSCHUNG.
 XX
 XX Frommer W, Ninnenmann O;
 XX
 XX WPI; 1995-171399/23.
 XX N-PSDB; AAQ88327.
 XX
 XX Plant ammonium transporter DNA in sense or anti-sense orientation -
 XX useful for transforming cells, esp. plant cells for prodn. of transgenic
 XX plants with altered nitrogen metabolism.
 XX
 XX Claim 3; Page 17-20; 23pp; German.

CC The ammonium transporter (AT) gene isolated from Arabidopsis thaliana
 CC (AAQ88327) is a preferred AT gene for use in generating transgenic plants
 CC ; the gene encodes the amino acid sequence in AAR74676. AT gene sequences
 CC can be incorporated into expression constructs in the sense orientation
 CC (for expression of translatable mRNA and hence synthesis of AT in the
 CC transgenic plants) or in the antisense orientation (resulting in
 CC antisense transcripts which inhibit synthesis of endogenous AT in the
 CC transgenic plants). Nitrogen metabolism is altered in the resulting
 CC transgenic plants; the changes in AT activity may also result in plants
 CC which are suitable for "low input" crop management or which can be grown
 CC in acid soils

XX SQ Sequence 501 AA;

Query Match 80.7%; Score 2129.5; DB 2; Length 501;
 Best Local Similarity 80.9%; Pred. No. 8.6e-202;
 Matches 407; Conservative 42; Mismatches 39; Indels 15; Gaps 7;

QY 5 ACPAQALQLLGNPTDASAAASLTCGHFAAVDSKFDVTAFAVDNTYLLFSAYLVFSMQL 64
 DB 2 SCSATDLAVLLGNP--ATAAANYICGQLGVNKFIDTAIDNTYLLFSAYLVFSMQL 58
 QY 65 GFAMLCAGSVRAKNTNMIMLTNVLDAAGLFFYLFGFAFAFGSPSNGFIKHFGLKDI 124
 DB 59 GFAMLCAGSVRAKNTNMIMLTNVLDAAGLFFYLFGFAFAFGSPSNGFIKHFGLKDI 118
 QY 125 PSSSYDYSLYQWAFIAAAGITSGSIAERTQFVAYLIYSSFLTGFFYPVSHWFSPD 184
 DB 119 PTASADYSNLYQWAFIAAAGITSGSIAERTQFVAYLIYSSFLTGFFYPVSHWFSPD 178
 QY 185 GWASAFKIT-DRLPSTGVIDFAGSGVVMVGGIAGLWGLALIEGRPMGRFDHAGRAVALRG 243
 DB 179 GWASPFRTDGLLFTSGAIDFAGSGVVMVGGIAGLWGLALIEGRPMGRFDHAGRAVALRG 238
 QY 244 HSASLVLTGTLFLLWFGYGNFPGSFNKILLTYGNSGNYGQWSAVGRTAVTTLAGSTAA 303
 DB 239 HSASLVLTGTLFLLWFGYGNFPGSFNKILLTY-ETGYNGQWSAVGRTAVTTLAGSTAA 297
 QY 304 LTTLFGKRVISGHNWNTDVCNGLLGGFAAITAGCSVVEPWAIVCGFVASIVLIACNLA 363
 DB 298 LTTLFGKRLLSGHNWNTDVCNGLLGGFAAITAGCSVVEPWAIVCGFVASIVLIACNLA 357
 QY 364 EKVKFDDPLEAAQLHGGCGTGWVIFTALFAKKEVYKVEVYGLGRAHGLLWGGGKLLA 421
 DB 358 EKLKTDDEPLEAAQLHGGCGTGWVIFTALFAKKEVYKVEVYGLGRAHGLLWGGGKLLA 417
 QY 422 HVIQILVIAGWSATMGPLFWGLNKLKLLRISSEDELAGMDMTRHGGFAVAY-EDDETHK 480
 DB 418 QLIQIIVITGWVSATMGPLFWGLNKLKLLRISSEDELAGMDMTRHGGFAVAY-EDDETHK 477
 QY 481 HGMQLRRVGNP-----NASSTPT 497
 DB 478 -AIQURRVEPRSPSPSGANTIPT 499

RESULT 3

AAG40620

ID AAG40620 standard; protein; 501 AA.

PR 20-MAY-1999; 99US-0135124P.
PR 21-MAY-1999; 99US-0135353P.
PR 24-MAY-1999; 99US-0135629P.
PR 25-MAY-1999; 99US-0136031P.
PR 27-MAY-1999; 99US-0136392P.
PR 28-MAY-1999; 99US-0136782P.
PR 01-JUN-1999; 99US-0137222P.
PR 03-JUN-1999; 99US-0137528P.
PR 04-JUN-1999; 99US-0137502P.
PR 07-JUN-1999; 99US-0137724P.
PR 08-JUN-1999; 99US-0138094P.
PR 10-JUN-1999; 99US-0138540P.
PR 10-JUN-1999; 99US-0138847P.
PR 14-JUN-1999; 99US-0139119P.
PR 16-JUN-1999; 99US-0139452P.
PR 16-JUN-1999; 99US-0139453P.
PR 17-JUN-1999; 99US-0139453P.
PR 18-JUN-1999; 99US-0139454P.
PR 18-JUN-1999; 99US-0139455P.
PR 18-JUN-1999; 99US-0139456P.
PR 18-JUN-1999; 99US-0139457P.
PR 18-JUN-1999; 99US-0139458P.
PR 18-JUN-1999; 99US-0139459P.
PR 18-JUN-1999; 99US-0139460P.
PR 18-JUN-1999; 99US-0139461P.
PR 18-JUN-1999; 99US-0139462P.
PR 18-JUN-1999; 99US-0139463P.
PR 18-JUN-1999; 99US-0139750P.
PR 18-JUN-1999; 99US-0139763P.
PR 21-JUN-1999; 99US-0139817P.
PR 22-JUN-1999; 99US-0139899P.
PR 23-JUN-1999; 99US-0140353P.
PR 23-JUN-1999; 99US-0140354P.
PR 24-JUN-1999; 99US-0140695P.
PR 24-JUN-1999; 99US-0140823P.
PR 29-JUN-1999; 99US-0140991P.
PR 30-JUN-1999; 99US-0141287P.
PR 01-JUL-1999; 99US-0141842P.
PR 01-JUL-1999; 99US-0142154P.
PR 02-JUL-1999; 99US-0142055P.
PR 06-JUL-1999; 99US-0142390P.
PR 08-JUL-1999; 99US-0142803P.
PR 09-JUL-1999; 99US-0142920P.
PR 12-JUL-1999; 99US-0142977P.
PR 13-JUL-1999; 99US-0143542P.
PR 14-JUL-1999; 99US-0143624P.
PR 15-JUL-1999; 99US-0144005P.
PR 16-JUL-1999; 99US-0144085P.
PR 16-JUL-1999; 99US-0144086P.
PR 19-JUL-1999; 99US-0144325P.
PR 19-JUL-1999; 99US-0144331P.
PR 19-JUL-1999; 99US-0144332P.
PR 19-JUL-1999; 99US-0144333P.
PR 19-JUL-1999; 99US-0144334P.
PR 19-JUL-1999; 99US-0144335P.
PR 20-JUL-1999; 99US-0144352P.
PR 20-JUL-1999; 99US-0144632P.
PR 20-JUL-1999; 99US-0144884P.
PR 21-JUL-1999; 99US-0144814P.
PR 21-JUL-1999; 99US-0145086P.
PR 21-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145085P.
PR 22-JUL-1999; 99US-0145087P.
PR 22-JUL-1999; 99US-0145089P.
PR 22-JUL-1999; 99US-0145192P.
PR 23-JUL-1999; 99US-0145145P.
PR 23-JUL-1999; 99US-0145218P.
PR 23-JUL-1999; 99US-0145224P.
PR 26-JUL-1999; 99US-0145276P.
PR 27-JUL-1999; 99US-0145913P.
PR 27-JUL-1999; 99US-0145918P.
PR 28-JUL-1999; 99US-0145919P.
PR 28-JUL-1999; 99US-0145951P.
PR 02-AUG-1999; 99US-0146386P.
PR 02-AUG-1999; 99US-0146388P.
PR 02-AUG-1999; 99US-0146389P.
PR 03-AUG-1999; 99US-0147038P.
PR 04-AUG-1999; 99US-0147204P.
PR 04-AUG-1999; 99US-0147302P.
PR 05-AUG-1999; 99US-0147192P.
PR 06-AUG-1999; 99US-0147303P.
PR 06-AUG-1999; 99US-0147416P.
PR 09-AUG-1999; 99US-0147493P.
PR 09-AUG-1999; 99US-0147935P.
PR 10-AUG-1999; 99US-0148171P.
PR 11-AUG-1999; 99US-0148319P.
PR 12-AUG-1999; 99US-0148341P.
PR 13-AUG-1999; 99US-0148565P.
PR 13-AUG-1999; 99US-0148684P.
PR 16-AUG-1999; 99US-0149368P.
PR 17-AUG-1999; 99US-0149175P.
PR 18-AUG-1999; 99US-0149426P.
PR 20-AUG-1999; 99US-0149722P.
PR 20-AUG-1999; 99US-0149723P.
PR 20-AUG-1999; 99US-0149929P.
PR 23-AUG-1999; 99US-0149902P.
PR 23-AUG-1999; 99US-0149930P.
PR 25-AUG-1999; 99US-0150566P.
PR 26-AUG-1999; 99US-0150884P.
PR 27-AUG-1999; 99US-0151065P.
PR 27-AUG-1999; 99US-0151066P.
PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 15-SEP-1999; 99US-0154018P.
PR 16-SEP-1999; 99US-0154039P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155139P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 06-OCT-1999; 99US-0157753P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158222P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 14-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.

PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.
Query Match 80.7%; Score 2129.5; DB 3; Length 510;
Best Local Similarity 80.9%; Pred. No. 8.8e-202;
Matches 407; Conservative 42; Mismatches 39; Indels 15; Gaps 7;
QY 5 ACPAPQLAQLGPNNTDASAAALICGHFAAVDSKFVDTAFAVDNTYLLFSAYLVFSMOL 64
Db 2 SCSATDLAVILGPN---ATAAANYICQGLGVNNKFIDTAFAIDNYLLFSAYLVFSMOL 58
QY 65 GFAMLCAGSVRAKNTMTNLTNVLDAAGGLFYLLFGFAFAFGSPNGFTGKHFGLKDI 124
Db 59 GFAMLCAGSVRAKNTMTNLTNVLDAAGGLFYLLFGFAFAFGSPNGFTGKHFGLKDI 118
QY 125 PSSSYDYSYFLYQWAFATAAGITSGSIAERTQFVAVLIYSSFLTGFPVYVSVSHWFSVD 184
Db 119 FRASADYNFLYQWAFATAAGITSGSIAERTQFVAVLIYSSFLTGFPVYVSVSHWFSVD 178
QY 185 GWASAFKIT-DRLFSTGVDFAGSGVHMVGGIAGLWGLALIEGPRMGRFDHAGRAVALRG 243
Db 179 GWASPFRTDGLLFTSTGAIDFAGSGVHMVGGIAGLWGLALIEGPRMGRFDHAGRAVALRG 238
QY 244 HSASLVVLGTFLLWFGWGENFGSPNKLITLVYSGNSGVYQWASVAGRTAVTTTLAGSTAA 303
Db 239 HSASLVVLGTFLLWFGWGENFGSPNKLITLVY-FGTYNQWASVAGRTAVTTTLAGCTAA 297
QY 304 LTTLFGRKVISGHMNVTDVNCGLLGGFAAITAGCSVVEPMAAIVCGFVASIVILIACNKLA 363
Db 298 LTTLFGRKLLSGHMNVTDVNCGLLGGFAAITAGCSVVEPMAAIVCGFVASIVILIACNKLA 357
QY 364 EKVKEDDPLEAQLHGGCGTWCVIPTALFAKKEVYKVEYG--LGRAHGLLMGGGKLLAA 421
Db 358 EKLKVDPLEAQLHGGCGGANGLIPTALFAKKEVYKVEYG--LGRAHGLLMGGGKLLGA 417
QY 422 HVIQILVIAGWYSATWGLFPLWGLANKLRLRISSDELAGMDMTRHGGFAYAY-EDDETHK 480
Db 418 QLIQIIVITWYSATWGLTFFLTKKQKLLRISSDELAGMDMTRHGGFAYAYFDDDESHK 477
QY 481 HGMQLRRVCP-----NASSPT 497
Db 478 -AIQLRRVPRSPSPSGANTTPT 499
RESULT 5
AAO26534
ID AAO26534 standard; protein; 494 AA.
XX AC AAO26534;
XX DT 18-FEB-2003 (first entry)
DE Wheat high affinity ammonium transporter protein.
XX DE Herbicide; ammonium transporter protein; herbicide; transgenic plant;
XX KW wheat.
XX OS Triticum aestivum.
XX PN US2002142390-A1.
XX PD 03-OCT-2002.
XX FF 28-DEC-2001; 2001US-00033109.
XX PR 28-AUG-1998; 98US-0098248P.
XX PR 27-AUG-1999; 99US-0038462S.
XX PA (ALLE/) ALLEN S M.
PA (RAFA/) RAFALSKI J A.

XX Allen SM, Rafalski JA;
XX WPI; 2003-102520/09.
DR N-PSDB; AAL53986.
XX Novel ammonium transporter polypeptide useful for identifying enzymatic
inhibitors, which is homologous to corn, soybean, wheat or rice ammonium
transporter polypeptides.
Claim 14; Page 17-18; 27pp; English.
The invention relates to a novel ammonium transporter protein comprising
90% homology based on the Clustal method compared to: a corn ammonium
transporter polypeptide of 183 or 63 amino acids; a soybean ammonium
transporter polypeptide of 500 or 486 amino acids; a wheat ammonium
transporter polypeptide of 494 or 470 amino acids; and a rice ammonium
transporter 497 amino acids fully defined in the specification. The
isolated polynucleotide is useful for selecting an isolated
polynucleotide that affects the level of expression of the ammonium
transporter polypeptide in a plant cell. The ammonium transporter protein
is useful for preparing antibodies which are useful for detecting the
transporter protein in situ in cells or in vitro in cell extracts, and as
targets to facilitate design and/or identify inhibitors of the enzymes
that are useful as herbicides. The isolated polynucleotide is also useful
for creating transgenic plants in which the polynucleotide is present at
higher or lower levels than normal, and for designing and producing
primer pairs which are useful in amplification or primer extension
reactions. This sequence represents the wheat high affinity ammonium
transporter protein of the invention
XX Sequence 494 AA;
Query Match 74.0%; Score 1954; DB 6; Length 494;
Best Local Similarity 74.8%; Pred. No. 2e-184;
Matches 374; Conservative 46; Mismatches 62; Indels 18; Gaps 5;
QY 3 LPACFAPQLAQLGPNNTDASAAALICGHFAAVDSKFVDTAFAVDNTYLLFSAYLVFSM 62
Db 1 MSATCAADLGLPLG---AAAANATDYLCNRFA-----DTSVNDSTYLLFSAYLVFSM 50
QY 63 QLGFAMLCAGSVRAKNTMTNLTNVLDAAGGLFYLLFGFAFAFGSPNGFTGKHFGLK 122
Db 51 QLGFAMLCAGSVRAKNTMTNLTNVLDAAGGLFYLLFGFAFAFGSPNGFTGKHFGLK 110
QY 123 DIPSSYDYSYFLYQWAFATAAGITSGSIAERTQFVAVLIYSSFLTGFPVYVSVSHWFS 182
Db 111 DMPQTGFDSYFFLQWAFATAAGITSGSIAERTQFVAVLIYSAFTGFPVYVSVSHWFS 170
QY 183 PDGWASAFKIT-DRLFSTGVDFAGSGVHMVGGIAGLWGLALIEGPRMGRFDHAGRAVAL 241
Db 171 VDGWASAAFTSGPLLFKSGVIDFAGSGVHMVGGIAGLWGLALIEGPRMGRFDHAGRAVAL 230
QY 242 RGHASLVVLGTFLLWFGWGENFGSPNKLITLVYSGNSGVYQWASVAGRTAVTTTLAGST 301
Db 231 KGHASLVVLGTFLLWFGWGENFGSPNKLITLVYSGNSGVYQWASVAGRTAVTTTLAGSV 290
QY 302 AALTTLFGRKVISGHMNVTDVNCGLLGGFAAITAGCSVVEPMAAIVCGFVASIVILIACNK 361
Db 291 AALTTLFGRKVISGHMNVTDVNCGLLGGFAAITAGCSVVEPMAAIVCGFVASIVILIACNK 350
QY 362 LAEKVDDPLEAQLHGGCGTWCVIPTALFAKKEVYKVEYG--LGRAHGLLMGGGKLLAA 421
Db 351 LAGRLKYDDPLEAQLHGGCGGANGLIPTALFAKKEVYKVEYG--LGRAHGLLMGGGKLLAA 410
QY 422 HVIQILVIAGWYSATWGLFPLWGLANKLRLRISSDELAGMDMTRHGGFAYAYEDDETHKH 481
Db 411 HVIQILVIAGWYSATWGLFPLWGLANKLRLRISSDELAGMDMTRHGGFAYAYEDDETHKH 470
QY 482 ---GMQLR-----RVGPNASS 494
Db 471 SVGGFMLRSQAQTRVEPAAAA 490

RESULT 6
AAG40621
ID AAG40621 standard; protein; 446 AA.
XX
AC AAG40621;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 50427.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; Genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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PR 04-MAY-1999; 99US-0132484P.
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AC AAG36234;

XX 18-OCT-2000 (first entry)
XX Arabidopsis thaliana protein fragment SEQ ID NO: 44376.

Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-00301439.

XX 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

XX 09-MAR-1999; 99US-0123548P.

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QY	241	LRGHSASLVVLGTFLLWFGWYGFNFSGFNKILLTYGNSGNTYQWMSAVGRTAVTTTLGAS	300	PR	14-MAY-1999;	99US-0134219P.
Db	181	LRGHSASLVVLGTFLLWFGWYGFNFSGFNKILLTY-ERGTYNGQWMSAVGRTAVTTTLGAC	239	PR	14-MAY-1999;	99US-0134221P.
QY	301	TAALTTLFGKRVISGHNTVDVCGILGGFAITAGCSVFEPMVAIIVCGFVASIVLIACN	360	PR	18-MAY-1999;	99US-0134370P.
Db	240	TAALTTLFGKRVISGHNTVDVCGILGGFAITAGCSVFEPMVAIIVCGFVASIVLIACN	299	PR	18-MAY-1999;	99US-0134768P.
QY	361	KLAEKVKFDDPLEAAQLHGGCGGTWGIPTALFAKEYYKVEYVG--LGRAHGLLMGGGKGL	418	PR	19-MAY-1999;	99US-0134941P.
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QY	419	LAHVIOILVIGWVSATWGLPFWGLNKLRLRISSEDELAGMDMTRHGGPAYAY-EDDE	477	PR	21-MAY-1999;	99US-0135353P.
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XX	Arabidopsis thaliana protein fragment SEQ ID NO: 50428.			PR	08-JUN-1999;	99US-0138094P.
DE	Protein identification; signal transduction pathway; metabolic pathway;			PR	10-JUN-1999;	99US-0138847P.
XX	hybridisation assay; genetic mapping; gene expression control; promoter;			PR	14-JUN-1999;	99US-0139119P.
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EF	25-FEB-1999; 99US-0121825P.			PR	18-JUN-1999;	99US-0139461P.
XX	05-MAR-1999; 99US-0123180P.			PR	18-JUN-1999;	99US-0139462P.
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PR	29-MAR-1999; 99US-0126785P.			PR	22-JUN-1999;	99US-0139817P.
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XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
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Best Local Similarity 82.5%; Pred No. 2, 1e-180;
Matches 363; Conservative 35; Mismatches 30; Indels 12; Gaps 6;

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DB 1 MCAGSVRAKNTNMIMLVNLDAAAGLFFYLLFGFAFAGSPNSNGFTGKHFFGLKDIPSS 60
QY 128 SYDYSVFLYQWAFATAAGITSGSTAEFTQFVAVLYSSFTGVPVYVWSHFWSPDGA 197
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DB 121 SPFRDGDLLFTSTGAIDFAGSGVHMVGGIAGLNGALIEGPRMGRPDHAGRAVALRGHSA 180
QY 247 SLAVLGTFLFWGTVGFPNPKLLTYGNSGNYGQWSAVGTATVTTLAGSTAALT 306
DB 181 SLVVLGTFLFWGTVGFPNPKLLTYGNSGNYGQWSAVGTATVTTLAGSTAALT 239
QY 307 LFGKRVISGHMNVTVDCNGLLGGFAATAGCSVVEPMAAIVCGFVASIVLACNKLAEKV 366
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DT 26-MAR-2002 (first entry)
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XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US009231.
XX
PR 23-MAR-2000; 2000US-0191637P.
PR 11-JUL-2000; 2000US-00614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSDB; ABL06525.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions.
XX
XX Disclosure; SEQ ID NO 14058; 21pp + Sequence Listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins (AB857737-
XX ABB72072). The sequence data for this patent did not form part of the
XX printed specification, but was obtained in electronic format directly
XX from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local Similarity 36.1%; Pred. No. 1, 3e-55;
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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:52:48 ; Search time 21 Seconds
(without alignments)
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Searched: 283366 seqs, 96191526 residues
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1973.5	74.8	504	2 T04529	probable ammonium
3	1953	74.0	514	2 T06583	ammonium transport
4	1919	72.7	514	2 A86671	ammonium transport
5	1792.5	67.9	533	2 T05441	probable ammonium
6	771.5	29.2	435	2 H72379	ammonium transport
7	715.5	27.1	498	2 AC1930	ammonium transport
8	711.5	27.0	468	2 A69468	ammonium transport
9	706	26.8	534	2 T15414	hypothetical prote
10	703	26.6	507	2 S76687	hypothetical prote
11	678.5	25.7	442	2 AD7801	ammonium transport
12	665	25.2	518	2 AD1930	ammonium transport
13	655	24.8	421	2 B84129	ammonium transport
14	579.5	22.0	622	2 T23804	hypothetical prote
15	569.5	21.6	541	2 S76017	hypothetical prote
16	523	19.8	439	2 B75487	ammonium transport
17	523	19.8	470	2 AE1930	ammonium transport
18	523	19.8	592	2 T15413	hypothetical prote
19	504.5	19.1	388	2 D6468	ammonium transport
20	503	19.1	448	2 T35667	ammonium transport
21	500	18.9	405	2 H96983	ammonium transport
22	496	18.8	477	2 H70747	probable ammonium
23	494	18.7	404	2 A36865	ammonium transport
24	492	18.6	401	2 AF1626	ammonium transport
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26	485	18.4	420	2 F64467	ammonium transport
27	471.5	17.9	449	2 AE2915	ammonium transport
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ALIGNMENTS

RESULT 1

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N:Alternate names: NH4+ transporter; protein T6G15.60
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 24-Nov-1999
C:Accession: T06653; S46226; S59843
R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X
submitted to the Protein Sequence Database, April 1999
A:Reference number: 215791
A:Accession: T06653
A:Molecule type: DNA
A:Residues: 1-501 <BEV>
A:Cross-references: EMBL:AL049656; GSPDB:GN00062; ATSP:T6G15.60
A:Experimental source: cultivar Columbia; BAC clone T6G15
R:Ninnemann, O.; Jauniaux, J.C.; Prommer, W.B.
EMBO J. 13, 3464-3471, 1994
A:Title: Identification of a high affinity NH(4)(+) transporter from plants.
A:Reference number: S46226; MUID:94341258; PMID:8062823
A:Accession: S46226
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-82, 'EP', 85-501 <NIN>
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R:Prommer, W.B.
submitted to the EMBL Data Library, January 1994
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A:Map position: 4
C:Superfamily: ammonium transport protein amt1
C:Keywords: ammonium transport; transmembrane protein

Query Match 80.7%; Score 2129.5; DB 2; Length 501;
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DB 2 SCSTADLAVLGPNTTASAAASLTCGHFAAVDSKFDVTAFAVDNTYLLFSAYLVFSMQL 58
QY 65 GFAMLCAGSVAKNTNMLTNVLDAAAGGLFYFLFGFAFGSPNSNGTIGKHFGLKDI 124
DB 59 GFAMLCAGSVAKNTNMLTNVLDAAAGGLFYFLFGFAFGSPNSNGTIGKHFGLKDI 118
QY 125 PSSSDYISYFLYQWAFAPAAAGITSGSIAERTOPVAYLLYSSFLTGCVYVYVSHWNSPD 184
DB 119 PTASADYSNFLYQWAFAPAAAGITSGSIAERTOPVAYLLYSSFLTGCVYVYVSHWNSVD 178

A:Residues: 1-435 <ARN>
A:Cross-references: GB:AE0001720; GB:AE000512; NID:94980906; PIDN:AAD35487.1; PID:94980906
A:Experimental source: strain MSB
C:Genetics:
A:Gene: TM0402
C:Superfamily: ammonium transport protein amt1

Query Match 29.2%; Score 771.5; DB 2; Length 435;
Best Local Similarity 38.2%; Pred. No. 4.1e-51;
Matches 166; Conservative 75; Mismatches 157; Indels 37; Gaps 9;

QY 42 DTAFAVDNTYLLFAYLVFSMQLGAFMLCAGSVRAKNTNMIMLTNVLDAAGGLFYLLFG 101
DB 26 DVGSLDMWVILISAALVFFMQAGFAMVESGFRKNTVNVLMKNLMDFAIGSVVFFIEG 85
QY 102 FAFAGSPSNGFIKGFHFFGLKDIPSSS---YDYSYFLYQWAFIAAAGITSGSIAERTQF 158
DB 86 YWINE-----GKH--PLTFDPSSTKEGLWDFAMWFMQAFAGTAATVSGMAERTKF 135
QY 159 VAYLIYSSFLTGFPVYVSHFWSPDQWASAFKITDRLFTGTVIDFAGSGVVMVGGIAG 218
DB 136 PAYLAYTGFTITGIYSVVGRIWG--GGW-----LAQGFIDFAGSTVHVSOGMAA 185
QY 219 LWGALIEPRMRPHAGRAVALRGHSASIVLGTFLFWGTVGFPNPGSFNKILLTYGNS 278
DB 186 MGSALLGPRGKYDSQGNPKPIGHNIPLAALGTFLFWGTFNGFGGS-----TLAGTN 240
QY 279 GNYQGWASAVRTAVTTLAGSTAAALTTLFQKRVISGHWNVDVCGNLLGGFAATAGCS 338
DB 241 G-----AIGMIILNTNLAATGALAAMVTVWAKYKPDASMTMGALAGLVAITAPCA 293
QY 339 VVEPWAAIVCGFVASIVLIACNKLAEKV-KPDDPLEAAQLHGGCGTGWVFTALPAKKEY 397
DB 294 VVSPVSSIIIGAGVIVVFAVEFDFKVLKIDDPVGAISVHGNGANGTLAVGLFAESKY 353
QY 398 VKEVYGLGRAHGLMGCGKLLAAHVLIQILVAGVVSATMGPLFWGLNKLKLRISSEDE 457
DB 354 AL-ASGMGDVNGLFFGGVHQLGVQFLGWSVFATVTVTSLFWFMTKKTIGLRVDRDIE 412
QY 458 LAGMDMTRHGGPAYA 472
DB 413 LKGLDIEHGMGYA 427

RESULT 7
AC1930
ammonium transporter alr0990 [imported] - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AC1930
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriiguchi, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.
DNA Rep. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AC1930
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-498 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA072947.1; PID:G17130336; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr0990
C:Superfamily: ammonium transport protein amt1

Query Match 27.1%; Score 715.5; DB 2; Length 498;
Best Local Similarity 34.4%; Pred. No. 8.7e-47;
Matches 169; Conservative 71; Mismatches 184; Indels 67; Gaps 10;

QY 24 AAASLICGFAAVDSKFDVT-----AFADVNTYLLFSAYLVFSMQLGAFMLC 70
DB 25 AIGSMVFAVFAPTVQAVDTPTLESSETIKLQISIDTTWLLSGLVLFPMQTGFAMLE 84

QY 71 AGSVRAKNTNMIMLTNVLDAAGGLFYLLFGFAPGSPSNGFIKGFHFFGLKDIPSS--S 128
DB 85 AGLVRQSRVVNTLLENFIDAAVTVLAWAVGFIAGTSGAGLFGIDTFFLSQLFGADGS 144
QY 129 Y-----DYSYFLYQWAFIAAAGITSGSIAERTQFVAVLIYSSFLTGFPVYV 176
DB 145 YPIGAFGSGTAATNTYTLFFQFAFAATATITSGNAGRTDFIGDLIYSAIMGALISYPII 204
QY 177 SHWFSPDQWASAFKITDRLFTGTVIDFAGSGVVMVGGIAGLWALIEGPR-----MGR 231
DB 205 VHNWNSNGW-----LGKLSYHDFPAGGSI VHTVGWTVLAVGAYLLGPRDPRPPMGK 255
QY 232 FDHAGRAVALRGHSASIVLGTFLFWGTVGFPNPGSFNKILLTYGNSGNYQGWASAVGT 291
DB 256 LPPA-----HNLALATLGTMLFWGTVGFPNPGS-----TLGTANPG-----LIGLV 296
QY 292 AVTTTLTAGSTAALTTLFGKRVISGHWNVDVCGNLLGGFAATAGCSVVEPWAAIVCGFV 351
DB 297 TINTTLAAGALAAALIFLYVRTGKMDLVYCLNGSLAGLVAITAPCAVVPWASVLIGLT 356
QY 352 ASIVLIACNKLAEKVDFDPLEAAQLHGGCGTGWVFTALPAKKEYVVEVYGLGRAHGL 411
DB 357 GGIADVLSGLIESLHDDPVGAFSVHGISGMMGTLSIGFLGQEELT-----LNQAGLL 411
QY 412 MGGGCKLAAHVLIQILVAGVVSATMGPLFWGLNKLKLRISSEDELAGMDMTRHGGFAY 471
DB 412 LGGGFDLLGQLMGIIVTTFVAFAPLWYGLKAMGHLRVNAEADRIDTIDTYEHGASVW 471
QY 472 --AYEDDETHK 480
DB 472 PDVYSVEELSK 482

RESULT 8
A69468
ammonium transporter (amt-2) homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C:Accession: A69468
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Overbeek, R.; Cotton, M.D.; Spriggs, T.; Ariach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: A69468
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-468 <KLE>
A:Cross-references: GB:AE000982; GB:AE000782; NID:92689305; PIDN:AAB89503.1; PID:9264880
C:Superfamily: ammonium transport protein amt1

Query Match 27.0%; Score 711.5; DB 2; Length 468;
Best Local Similarity 37.3%; Pred. No. 1.6e-46;
Matches 160; Conservative 62; Mismatches 186; Indels 21; Gaps 6;

QY 47 VDNVTYLLFSAYLVFSMQLGAFMLCAGSVRAKNTNMIMLTNVLDAAGGLFYLLFGFAPAF 106
DB 37 VDFVNALICGFLVFMQAGFAMLEAGFSRAKNTVNVLMKNLMDFAVGLAFPAVGFALMM 96
QY 107 GSPSNGFIKGFHFFGLKDIPSSSYDYS---YFLYQWAFIAAAGITSGSIAERTQFVAYLI 163
DB 97 GADWQGTAGTTGTWFL---AGESYDVSTIELWFFMLVFAATAATVSGSIAERPKFSVILV 153
QY 164 YSSFLTGFPVYVSHFWSPDQWASAFKITDRL-FSTGVIDFAGSGVVMVGGIAGLWGA 222
DB 154 YSAVVSIVYIYTGHWLWG--GGMLSSSEFMVKGGLDFFAGSGVHAIQGYITAAAV 212
QY 223 LIEGPRMRPHAGRAVALRGHSASIVLGTFLFWGTVGFPNPGSFNKILLTYGNSGNY 282

Db 213 MLGPRKLYDSQGNPRAIPQHNLAFAVIGTFFILMFQWFGFNAGS-----TLS 260
QY 283 QOWSAVGRKTAATTTLAGSTAALTTLFGRVVISGHNWNTDVCNGLLGGFAAITAGCSVVEP 342
Db 261 AHELRSVSIASNTNLAAAGAVTAMAITLWRNGKPDVGMTCTCGAVAGLVAITAPCAWQP 320
QY 343 WAAIVCGFVASIVLLACNKLAEKVKDDPLEAAQLHGGCGTGWIVFTALPAKKEYKVEY 402
Db 321 WSSVVIIGTIGATYGYWLEKRGDDVVGAIPTVHFGSGTGLIALGIFADGSGYLYAT 380
QY 403 GLGRAHLLGGGKILAAHVQIQLVIAGWVSATMGPLFGLNKLKLLRAISSEDELAMG 462
Db 381 ESPLVTGLLYNGW-FTIVQLISAIVNFAFGTGFALFWLKKVIGIRVSPSEEMGLGD 439
QY 463 MTRHGGFAY 471
Db 440 IAEHAAYAY 448

RESULT 9
T15414
hypothetical protein C05E11.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 18-Feb-2000
C/Accession: T15414
R/Geisel, C.
submitted to the EMBL Data Library, April 1996
A/Description: The sequence of C. elegans cosmid C05E11.
A/Reference number: Z18347
A/Accession: T15414
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-534 <GBI>
A/Cross-references: EMBL:U53338; NID:G1255840; PID:G1255843; PIDN:AAA96191.1; GSPDB:GN00
A/Experimental source: strain Bristol N2; clone C05E11
C/Genetics:
A/Gene: CESP:C05E11.4
A/Map position: X
A/Introns: 43/1; 151/1; 182/3; 229/3; 339/2; 394/3; 423/3; 490/1
C/Superfamily: ammonium transport protein amt1

Query Match 26.8%; Score 706; DB 2; Length 534;
Best Local Similarity 36.0%; Pred. No. 4.9e-46;
Matches 164; Conservative 74; Mismatches 185; Indels 32; Gaps 9;

QY 41 VDTAF--AVDNTYLLFSAYLVFMSQLGFAMLCAGSVRAKNTNIMLTNVLDAAGGLFY 98
Db 21 LETGFENVNSFFLCSMALIIFPMQCGFAYLEAGAVRSKNTTNILKNLLDSCIIQYW 80
QY 99 LFGFAPAGSPSNG---FIKHFEGKIDIPSSSYDYSELYOWAFALAAAGITSGSIAER 155
Db 81 AIGWALYGSQGVNLFVGHOSFFL---SGFSDIPRFQYVFSATAATVSGAVAR 136
QY 156 TQFVAYLYSSFLTGTVYVVSWMFSPDGWASAFKITDRLSTGTVIDFAGSGVVMVVG 215
Db 137 CEFITYTVTVISTFIYVPLTHWGTENGW-MAKGITSIIDTKYDDFAGSGLVHLGG 195
QY 216 IAGLWGLALIEGPMGRF--DHAGRAVALRCHSASLVLTGLFMGWTGTFNPKILL 273
Db 196 SIGFLAWIMGPIKGFPPDEDEDEIIGHVSFTFALGGFILMFGLAFNGGSVASI-- 253
QY 274 TYGNSGNYQOWSAVGRTAVTTTLAGSTAALTTLFGRVVISGHNWNTDVCNGLLGGFAA 333
Db 254 -----SHAGDGTVALAMINTILSGAFAALIYGVHYVHQKWTLLLTINACLSGMVA 307
QY 334 TAGCSVVEPWAIVCGFVASIVLLACNKLAEKVKDDPLEAAQLHGGCGTGWIVFTALPA 393
Db 308 CAGCKNEPWAIVCGFVASIVLLACNKLAEKVKDDPLEAAQLHGGCGTGWIVFTALPA 367
QY 394 KKEVYKVEYVGLGRAHLLGGGKILAA-----HVIQLVLIAGWVSATMGPLFGLNKL 447
Db 368 ---HGGVAYALADAVSGAKNSGDLTQAFAQLGWQMICALAIANSGLWMLPIFWILKKT 424

QY 448 KLLRISSEDELAMDMTRHGGFAYAYEDDETHKHG 482
Db 425 GKLRVSEVEINGLDVKHGEAMAYPL---RAYGHG 456

RESULT 10
S76887
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C/Species: Synechocystis sp.
A/Variety: PCC 6803
C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C/Accession: S76887
R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A/Reference number: S74322; MUID:97061201; PMID:8905231
A/Accession: S76887
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-507 <KAN>
A/Cross-references: EMBL:D64004; GB:AB001339; NID:G1001701; PIDN:BA010631.1; PID:G12084;
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C/Superfamily: ammonium transport protein amt1

Query Match 26.6%; Score 703; DB 2; Length 507;
Best Local Similarity 36.2%; Pred. No. 7.9e-46;
Matches 160; Conservative 63; Mismatches 173; Indels 46; Gaps 8;

QY 51 YLFSAYLVFSMQLGFAMLCAGSVRAKNTNIMLTNVLDAAGGLFYLFQFAFAGSPS 110
Db 92 WLIIAAILVIFWVAGFGMLETGLCRQKNAVILTKNLIVPALATIAYWAGFSLMFGSSG 151
QY 111 NGFI-----GKHF-GLKIDIPSSSYDYSELYOWAFALAAAGITSGSTAERTQFVAY 161
Db 152 NPFVGGGFFLSDHTNYGLSPFPEGLPVAVFFLQVAFSATAATVSGVAERIKFNEF 211
QY 162 LIYSSEFLTGTVYVVSWMFSPDGWASAFKITDRLSTGTVIDFAGSGVVMVVGGLW 221
Db 212 LIFSLLVGLIAYPTIGHVWVDAGW-----LYTWGFMDFAGTIVVHSGVGMWALAG 262
QY 222 ALIEGPMRPFHAGRAVALRCHSASLVLTGLFMGWTGTFNPKILLTIVGNSGY 281
Db 263 AFLGLERLKFVD-GRPGAIPGHNMGMFAMLOCLLWIGWFGFNFGS-----Q 308
QY 282 YGOWSAVGRTAVTTTLAGSTAALTTLFGRVVISGHNWNTDVCNGLLGGFAAITAGCSVVE 341
Db 309 LAADQACAVIATTNLAASAGCLTATFTSLKDKGKPDLTWINGVLAGLVITAGCAGVS 368
QY 342 PWAIVCGFVASIVLLACNKLAEKVKDDPLEAAQLHGGCGTGWIVFTALPAKKEYKVEV 401
Db 369 YWGSVLIIGIAGILVYVSVAFFDKIKIDDPVGAISVHLVNGVWGTAVGFFNMEK----- 423
QY 402 YGLGRAHLLGGGKILAAHVQIQLVIAGWVSATMGPLFGLNKLKLL-RISEDELAG 460
Db 424 -----GLFYGGGINQLLIQIVGILAI-GAFTAFSVVWAILKQTMGIRVSGEEMIG 475
QY 461 DMTRHGGFAYAYEDDETHKHG 482
Db 476 LDIGEHGMEAYTGFVKETDSFG 497

RESULT 11
S74801
ammonium transport protein - Synechocystis sp. (strain PCC 6803)
N/Alternate names: protein sll1017
C/Species: Synechocystis sp.
A/Variety: PCC 6803
C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C/Accession: S74801
R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asanizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,

A:Residues: 1-421 <ST0>
 A:Cross-references: GB:BA0001520; GB:BA000004; NID:g10176401; PIDN:BA07553.1; GDB:1000000000
 A:Experimental source: strain C-125
 C:Genetics:
 A:Gene: BH3834
 C:Superfamily: ammonium transporter nrgA

	Query Match	24.8%;	Score 655;	DB 2;	Length 421;
	Best Local Similarity	32.9%;	Pred. No. 2.9e-42;		
	Matches 153;	Conservative 69;	Mismatches 175;	Indels 68;	Gaps 13;

QY	41	VDTAFADVNTYLFSAFYLPFSNQLGFAMLCAGSVEAKNTNIMLTNVLDAAGSLFYFLF	100
	:	:::	
	:	:::	
Db	1	MSDIALMDNWMIMLCVLLMQGGFILLIAGSTRMKNAGHIAKTIPTVGIASLVYVAV	60
QY	101	GFAPAGSPSNGFIG--KHFFGLKDIIPSSVDYSY-----FLYQWAFATAAAGIT	148
	:	:::	
Db	61	GWGTYGE-GNAIFGLSDFFPG-----DYSTAEGLVGSVDFFQLMFAAIALTIA	110
QY	149	SGSIAERTQFVAVLYIYSSELTGFVYVPVSHFWSPDGWASAFKITDKLFTSGVIDFAGSG	208
	:	:::	
Db	111	PGGPAERAKLSVILFAVLSFVYPIVAHMTWG-DGW-----LADLGKQDFAGST	160

QY 209 VVHVGGIAGLWALIEGPRMGRFDHAGRAVALRHGSASLVVLGTFLLWFGWYGFNPGSF 268
Db 161 VVHLTGAMGALAAATILLKRLGKYNKDGSMNDIQHNQVYFALGVLLWVGWGFNAGST 220
QY 269 NKILLTYGNSGNYGWSAVGRTATVTTLAGSTAALTLFGKRVISGHWNVDVCGLLG 328
Db 221 LEVADAF-----FGVALNTQAAAGAAVAAAFIAWALSGKADVPPTTLNGALA 268
QY 329 GFAAITAGCVVPEPAAIIVCGFVASIVLIACNKLAEKVKFDDPLEAAQLHGGCGTGWVIF 388
Db 269 GLVAITASCFAVPAAVAVVIGVGLVYFVSKFPDKAKIDDPFALSVRHGVAGVGTLS 328
QY 389 TALFAKVEYKVEYGLGRHGLLMGGGKLLAAHVQILV-----TAGWY-----SATM 437
Db 329 TGFFATPE-LAEMNG-GQA-GLFYGGGFAQLGVQTLSSVACGVFAFTASYLLLVCKSVL 385
QY 438 GPLFWGLNKLKLLRISSEDELAGMDTMRHGGFAYAYEDETTHKG 482
Db 386 GG-----LRVTEEEIIGLDSHSGSYGYPESMPGSEKSG 420

RESULT 14
T23804
hypothetical protein M195.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T23804
R:Burton, J.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z19801
A:Accession: T23804
A:Status: preliminary;
A:Molecule type: DNA
A:Residues: 1622 <WIL>
A:Cross-references: EMBL:Z66498; PIDN:CAA91293.1; GSPDB:GNO00020; CESP:M195.3
A:Experimental source: clone M195
C:Genetics:
A:Gene: CESP:M195.3
A:Map position: 2
A:Introns: 18/1; 55/1; 152/1; 315/1; 379/3; 421/3; 465/2; 508/1; 554/1

Query Match 22.0%; Score 579.5; DB 2; Length 622;
Best Local Similarity 31.8%; Pred. No. 2.4e-36;
Matches 156; Conservative 86; Mismatches 169; Indels 79; Gaps 19;

QY 14 LLGPNTT--DASAAGSLICGHPAAYD-SKFDVTAFAVDNTVLLFSAYLVFSMQLGFAMLC 70
Db 1 MAGPEGSIFNASMQIVQIHHYAGSVTPVDKLYQDDAVLISSFIIFTHSGFGLLE 60
QY 71 AGSVRAKNTNIMLTNVLDAAGGLFYILFGPAPAF-----SPSNGFIKHF----- 118
Db 61 SGSVSARDEVNIMKVNVDVDFGLSYMSGCGFGSYGDIPEWRNPYVG-FKFFYDPTRD 119
QY 119 FGLKD-IPSSSYDYSLYQWAFATAAGITSGSIAERTQFVAYLIYSSFLTGFVPVWS 177
Db 120 YGTREINQEGWSYAFQLSLATASTIVSGVAERAKLSYLLGCVI-LIQALPA 178
QY 178 HWFSPDGNASAPKIIDTLRFSTGVIDFAGSVVHVGVIAGLWALIEGPRMGRFDHAGR 237
Db 179 HWVMDXEG-----VFYKXGVWDFAGCSAVHLVGGIIGLIATVFLKPRNRFNEDS- 228
QY 238 AVALRHGSASLVVLGTFLLWFGWYGFNPGSFNKLITTYGNSGNYGWSAVGRTAVTTTL 297
Db 229 --VHQSSPTNALLGTFLLWFGWYGFNPGS-----VWGIG-----GRWRLGARAAVATIM 277
QY 298 A---GSTAALTTLFGKRVISGHWNVDVCGLLGFAAITAGCSVVEPAAIIVCGFVASI 354
Db 278 ASIGGGATAITISFVK---TKLQVNFNLNGLISLTSIVSITAICAVSRPWHALVIGSISV 334
QY 355 VLTACNKLAEKVKFDDPLEAAQLHGGCGTGWVIFALFAKVEYKVEYGLGRA----HGL 410
Db 335 FSIAVLPLDLRLHIDDPVGIPIHLTSLTWSMGIAVGIPEEDKY-----LGSATNNRSGL 389

QY 411 LMGGGKLLAAHVQIILVIAGW-----SATMGEL-FWGLNKLKLLRISSEDE 457
Db 390 LVNSSEFEL-----WVQLQCTAAIIVSATTTGFLALFLISKPSPLGLRVTDYEE 437
QY 458 LAGMDTMRH 467
Db 438 QIGADVIEHG 447

RESULT 15
S76017
hypothetical protein - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S76017
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201; PMID:8905231
A:Accession: S76017
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-541 <KAN>
A:Cross-references: EMBL:D64006; GB:AB001339; NID:q1001291; PIDN:BAAL0864.1; PID:q100137
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Superfamily: ammonium transport protein amt1

Query Match 21.6%; Score 569.5; DB 2; Length 541;
Best Local Similarity 33.2%; Pred. No. 1.2e-35;
Matches 153; Conservative 58; Mismatches 191; Indels 59; Gaps 12;

QY 46 AVDTYILFSAVLVFSMQLGFAMLCASVRKNTNMTNVLDAAGGLFYILFGPAPA 105
Db 3 STDLMLLLCAGLVFFMQAGFCLESGLTRSKNSINVAIKNFADFGLISVALFWSFGFSIM 62
QY 106 FGSPNGSIGKHFFGLKIDIPSSSYDYSLYQWAFATAAGITSGSIAERTQFVAYLIYS 165
Db 63 FGLSGGWMGTG-YSFVDVGGEPTLAVFFLQAMFCGTATTIISGAAERLKFSAYLLVA 121
QY 166 SLTGFVYVYVSHWF-----SPDGWASAFKIDTLFSTGVIDFAGSVVHVG 215
Db 122 GLASGLIYFLFGDMAWNGLATVAGIETGGW-----LENLGFDFAGSTVHVSVA 172
QY 216 IAGLWGLIEGPRMGRFDHAGRAVALRHGSASLVVLGTFLLWFGWYGFNPGSFNKLITTY 275
Db 173 WIGLATILVVGPRQGRFPKTKLKIQSNWPFSLGTLILWFGWLGFGNGS-----TF 226
QY 276 GNSGNYGWSAVGRTAVTTTLAG-----STAALTTLFGKRVISGHWNVDVCGLLGGA 331
Db 227 GLTPEVPG-----INVNTVLAVGGMLMAGLISLLQDKI-----QVEPLMNGSLAGLV 275
QY 332 ATTACGSVVEPAAIIVCGFVASIVLIACNKLAEKVKFDDPLEAAQLHGGCGTGWVIF 391
Db 276 AITASANVMTPIAMVIGATGSAIAYLVGKMLHWGVDDDAVAVHGGAGVGTLCVGL 335
QY 392 PAKVEYKVEYGLGRAHGLLMGGGKLLAAHVQILVIA-GWVSATMGPLFWGLNKLKLL 450
Db 336 FQQLPLVDT--GLNRWQOC-----GVQLLIGVCTLWAFGLAWVFLTL-----LNRVFAL 383
QY 451 RISSEDELAGMDTMRHGGFAYAYE-----DDETHKGMLR 486
Db 384 RISPEDEIGLNVSEHQATTETTELFWMDRQAKTHDLSLR 424

Search completed: March 9, 2004, 11:56:07
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 9, 2004, 11:52:49 ; Search time 22 seconds
(without alignments)
1173.318 Million cell updates/sec

Title: US-10-033-109-4

Perfect score: 2639

Sequence: 1 MSIPACPAEQLAQLIGPNTT.....HGMLRRVGNASSTPTTDE 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/1aa/5A COMB.pgp:*
2: /cgn2_6/ptodata/2/1aa/5B COMB.pgp:*
3: /cgn2_6/ptodata/2/1aa/6A COMB.pgp:*
4: /cgn2_6/ptodata/2/1aa/6B COMB.pgp:*
5: /cgn2_6/ptodata/2/1aa/FACTUS COMB.pgp:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pgp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2129.5	80.7	501	4	US-08-635-967-2
2	488	18.5	470	4	US-09-328-352-5397
3	468	17.7	433	4	US-09-543-681A-6105
4	450	17.1	439	4	US-09-489-039A-12960
5	442	16.7	455	4	US-09-252-991A-23745
6	441	16.7	431	4	US-09-328-352-4217
7	420.5	15.9	464	4	US-09-252-981A-18525
8	406.5	15.4	437	4	US-09-134-001C-3907
9	203.5	7.7	361	4	US-09-134-000C-5907
10	193	7.3	223	4	US-09-107-532A-3674
11	182	6.9	224	4	US-09-107-532A-4102
12	136	5.2	443	4	US-09-489-039A-9335
13	121.5	4.6	490	4	US-09-489-039A-9610
14	119.5	4.5	517	4	US-09-252-981A-19322
15	119	4.5	557	4	US-09-252-981A-18216
16	117.5	4.5	472	3	US-09-354-129-2
17	117.5	4.5	472	4	US-09-504-357-2
18	113	4.3	471	4	US-09-252-991A-22393
19	111.5	4.2	481	4	US-09-252-991A-27157
20	109.5	4.1	470	4	US-09-328-352-6912
21	108	4.1	1216	4	US-09-134-000C-5130
22	107.5	4.1	391	4	US-09-489-039A-9791
23	106.5	4.0	306	4	US-09-328-352-5398
24	106.5	4.0	472	4	US-09-489-039A-13479
25	106.5	4.0	678	4	US-09-252-991A-20202
26	104	3.9	463	4	US-09-252-991A-29935
27	104	3.9	656	4	US-09-543-681A-7550

28	104	3.9	657	4	US-09-252-991A-27682	Sequence 27682, A
29	103	3.9	452	4	US-09-543-681A-6544	Sequence 6544, A
30	102.5	3.9	339	4	US-09-107-532A-4304	Sequence 4304, A
31	102.5	3.9	351	4	US-09-489-039A-12237	Sequence 12237, A
32	102.5	3.9	417	1	US-08-553-888A-3	Sequence 3, Appl1
33	102.5	3.9	457	4	US-09-489-039A-9693	Sequence 9693, A
34	102	3.9	467	4	US-09-489-039A-8037	Sequence 8037, A
35	102	3.9	512	4	US-09-540-236-3548	Sequence 3548, A
36	101.5	3.8	499	4	US-09-134-001C-5370	Sequence 5370, A
37	101	3.8	396	4	US-09-543-681A-5161	Sequence 5161, A
38	99.5	3.8	352	4	US-09-489-039A-8296	Sequence 8296, A
39	99	3.8	513	4	US-09-489-039A-12877	Sequence 12877, A
40	98.5	3.7	459	4	US-09-252-991A-22668	Sequence 22668, A
41	98.5	3.7	482	4	US-09-328-352-6084	Sequence 6084, A
42	98	3.7	389	4	US-09-489-039A-7563	Sequence 7563, A
43	98	3.7	455	4	US-09-489-039A-9942	Sequence 9942, A
44	97.5	3.7	439	4	US-09-172-952-14	Sequence 14, Appl1
45	97	3.7	421	4	US-09-489-039A-7699	Sequence 7699, A

ALIGNMENTS

RESULT 1

US-08-635-967-2
; Sequence 2, Application US/08635967
; Patent No. 6620610
; GENERAL INFORMATION:
; APPLICANT: FROMMER, Wolf-Bernd
; APPLICANT: NINEMAN, Olaf
; TITLE OF INVENTION: DNA SEQUENCES FOR AMMONIUM TRANSPORTER,
; TITLE OF INVENTION: PLASMIDS, BACTERIA, YEASTS, PLANT CELLS AND PLANTS
; TITLE OF INVENTION: CONTAINING THE TRANSPORTER
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen, LLP
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: PCT/EP 94/03499
; APPLICATION NUMBER: US/08/635,967
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP 94/03499
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 37 597.9
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weillman, Edward
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/951-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-635-967-2

Query Match 80.7%; Score 2129.5; DB 4; Length 501;

QY 445 NKLLRISSEDELAGMDTRHGGPAY 471
Db 405 DKLVGLRVQEBEHDGLDITTHGERAY 431

RESULT 4

US-09-489-039A-12960
Sequence 12960, Application US/09489039A

Patent No. 6610835

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 12960

LENGTH: 439

TYPE: PR

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-12960

Query Match 17.1%, Score 450; DB 4; Length 439;

Best Local Similarity 29.3%; Pred. No. 1.6e-39;

Matches 130; Conservative 69; Mismatches 177; Indels 68; Gaps 15;

QY 48 DNTYLLFSAYLVFSMOL-GFAMLCAGSVRAKNTNMILTNVLDAAGGL---FVYLRGFA 103

Db 42 DNAFMICHTALVLFMTIPGIALFYGLIRGNVLS-MLTQVI--VTFGLVCVLIWIGYT 98

QY 104 FAFGSPSGFIGHKHPG-----LKDIPSSSYDYSLYQWAFAPAAAGITGSI 152

Db 99 LAFGT-----GGSPFGSDWMLKNIELKALMGTFYQYIHVAFGSPACITVGLIVCAL 152

QY 153 AERTQFVAVLYYSSFLTGFPYVPSHWFSPDGWASAFKIDRLPSTGVIDFAGSGVVM 212

Db 153 AERIRSAVLIFVVMWTLVSYPHAWWG-----GGLATHGALDFAGTGVVHI 202

QY 213 VGGIAGLALGALIEGRMGRFDHAGRAVALRHSASLVVLGTFLFWGFGNPGSPFNKIL 272

Db 203 NAAVAGLVGAYMMGKRVG---FGKE-APKPHNLPWFTGTAILVGVWFGFNAGSA---- 253

QY 273 LTVGNSGNYGQWSAVGRTA---VTTILAGSTAALTTLFGKRVISGHWNVTVCNGLLG 328

Db 254 -----SAANEIALAFVNTVVATAAAILAWTFGEWALRGKPSLLGACSGAIA 300

QY 329 GFAAITAGCSVVEPMAAIVCGFVASIVLI-ACNKLAEKVKFDPLEAAQLHGGCGTGWVI 387

Db 301 GLVGVTTPACGYIGVGCALLIVGIASGLAGIWTALKRWLVRVDDPCDVFVGVHGVGIVGCI 360

QY 388 FTALPAKKEVKEVYGLGRAHGLMGGGKLLAAHVQILVIAGWVSATMTGFLFWGLNKL 447

Db 361 LTGIFA----ATSLGVGVGAEGVTM-GHOLLVQLESIAITVWWSGWAFIG--YKVDMT 413

QY 448 KLLRISSEDELAGMDTRHGGPAY 471

Db 414 VGLRVPEEQEREGLDVNSHENAY 437

RESULT 5

US-09-252-991A-23745

Sequence 23745, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

PNEUMONOSIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23745

LENGTH: 455

TYPE: PR

ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23745

Query Match 16.7%; Score 442; DB 4; Length 455;

Best Local Similarity 27.8%; Pred. No. 1.3e-38;

Matches 125; Conservative 68; Mismatches 150; Indels 66; Gaps 12;

QY 48 DNTYLLFSAYLVFSMOL-GFAMLCAGSVRAKNTNMILTNVLDAAGGLFYFLFGPAPAF 106

Db 46 DTAWMLISTALVLLMTIPGLALFYGGWVRKKNVLISMMQCFAITGLITILWVVGYSLAF 105

QY 107 GSPS-----NGFIG---KHFF-----GLKDIPSSSYDYSLYQWAFAPAAAGITS 149

Db 106 DTTGMEKGVLENFNSFVGGLDKAPLSGLTADGLTSATALFPESVFITFQMTFAITPALIV 165

QY 150 GSIARTQFVAVLYYSSFLTGFPYVPSHWFSPDGWASAFKIDRLPSTGVIDFAGSGV 209

Db 166 GAFARMKFSAMLIFMAVWFTVVYAPIAHVMVSGDG-----ALMMDWGVLDFAGGTV 217

QY 210 VHMVGIIAGLALGALIEGRMGRFDHAGRAVALRHSASLVVLGTFLFWGFGNPGSPFN 269

Db 218 VHINAGIAGLVACVLGKRGY-----PTTPMAHNLGYTLVGAAMLWICWFGFNAGS-- 270

QY 270 KILLTYGNSGNYGQWSAVGRTATVTTILAGSTAALTTLFGKRVISGHWNVTVCNGLLG 329

Db 271 -----AAAAAN-----GTAGWMLVTQIATAAALAWMFAEWITHGKPSALGIASGVAG 319

QY 330 FAAITAGCSVVEPMAAIVCGFVASIV-LIACNKLAEKVKFDPLEAAQLHGGCGTGWVIF 388

Db 320 LVAITPAAGTAGMGALVIGLASGVICFFAATSLKALKYDDSLDADFVGHAVGVIGALL 379

QY 389 TALPAKKEVKEVYGLGRAHGLMGGGK---LLAAHVQILVIAGWVSATMTGFLFWGLN 445

Db 380 TGIFAAPS-----LGFGSVEDIGAQFFVQKGVAFVVVYTAVVTFVILK 424

QY 446 KKLK---LRISSEDELAGMDTRHGGPAY 471

Db 425 VLDLVNGLRVTEEBEAVGLDLALHNERGY 453

RESULT 6

US-09-328-352-4217

Sequence 4217, Application US/09328352

Patent No. 6562958

GENERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 4217

LENGTH: 431

TYPE: PR

ORGANISM: Acinetobacter baumannii

US-09-328-352-4217

Query Match 16.7%; Score 441; DB 4; Length 431;

Best Local Similarity 29.6%; Pred. No. 1.5e-38;

Matches 132; Conservative 66; Mismatches 176; Indels 72; Gaps 13;

QY 38 SKFVDTAFA-VDNITYLLFSAYLVFSMQLGFAMLCAGSVRAKNTNMILTNVLDAAGGLF 96

Db 30 STFFEHAMQNDLFFLLGAVLVAMHAGFAFLGTGVRHKNQVNAKSKILTDPAISAIA 89
QY 97 YLFGFAFAGSPNGFICKHFGKIDIPSSSYDS-----YELQWAFATAAGITSGSI 152
Db 90 YFPVGYIISY-----GQHFHFGTGLSDHGNLMRCFFLLTFAAIPA--IISGGI 139
QY 153 AERTQVAVLIYSSFLTGTVYVWVSHWSPDGMASAFKITDRLFSTGVDFAGSGVYHM 212
Db 140 AERAKRSQAIATLALVALVYFFEGYMW--NGNYGLQKLETTFFGAHFDFAGSVVHA 197
QY 213 VGGIAGLWALIEGPRMGRFDHAGRAVALRHGASLVLTGTFLLWFGYNGPSPFNKIL 272
Db 198 MGGWIALAAVILIGARSRYKDKGRVSARPPSSIPFLALGWSLIVFGFNVMSAQRV- 256
QY 273 LTYGNSGNYQWSAV-GRATVTTTLA--GSTAALTTLFGKRVISGHWNVDVNCNGLIG 329
Db 257 -----DAISGLVAINSLMAMVGGITANAI-----GKNDPGFLHNGPLAG 296
QY 330 FAATAGCSVPEPAAIVCGFVASIVLIACNKLAE-KUKFDDPLEAAQLHGGCGTGWVIP 388
Db 297 LVAICAGSDIVHPVSALVTGGAGAMFVYLYTQNKLVDDVLGVWPLHGVCGAFGGIA 356
QY 389 TALPFAK-----BYKEVYGLGRAHGLLMGGGKLLAAHVIGILVIAGWVSATMGL 440
Db 357 VGIFQKWLGLGVSFISQLGTALAIALAGG-----FIVYGILKATIG-- 403
QY 441 FWGLNKLKILRISSEDELAMDMTRH 466
Db 404 -----IRLSQDEFRGADLSIH 420

RESULT 7
US-09-252-991A-18525
; Sequence 18525, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18525
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18525

Query Match 15.9%; Score 420.5; DB 4; Length 464;
Best Local Similarity 31.18; Pred. No. 2.6e-36;
Matches 137; Conservative 58; Mismatches 178; Indels 67; Gaps 14;

QY 49 NT-YLLFSAYLVFSQGLFAMLCAGSVRAKTNMILTNVLDAAAGLFPYLLFGFAFAG 107
Db 78 NTLFILLGAVMLAMHAGFAFLGTGVRHKNQVNAKSKILSDPAISALAYFFVGYIAYG 137
QY 108 SPNGFICKHFGKIDIPS-----SSYDSYFLYQWAFATAAGITSGIAERTQFVAY 161
Db 138 VT-----FFH-----PAALATVDSGLVVKFFLLTFAAIPAIIISGIIERARFGPQ 185
QY 162 LIYSFSLTGFPYVWVSHWSPDGMASAFKITDRL---FSTGVDFAGSGVYHMGVIAG 218
Db 186 LCATALIVAFVYP-----FFGELVWNGNFGLEQWKLFCAPDHPDAGSVVHALGMLA 240
QY 219 LWGALIEGPRMGRFDHAGRAVALRHGASLVLTGTFLLWFGYNGPSPFNKILLTYGNS 278
Db 241 LAAVLLLSRNGRY-RDGLVMAAPSSIPFLALGWSLIIIGWFGFNVMSAQTLA----- 293

QY 279 GNYTQWSAVGRTAVTTTLA--GSTAALTTLFGKRVISGHWNVDVNCNGLLGFAAITAG 336
Db 294 -----GVSLVAVNSLLAMVGTM-----SLLIGRNDPGFLHNGPLAGLVAVCAG 339
QY 337 CSVPEPAAIVCGFVASIVLI-ACNKLAEKVKFDDPLEAAQLHGGCGTGWVIPFALFAK 395
Db 340 SLDMPHICATATGLVAGALFWMAFTATQVRKIDDDVLGVWPLHGLGVWGGIACGIFGQ 399
QY 396 EYVKEVYGLGRAHGLLMGGGKLLAAHVIGILVIAGWVSATMGLPFWGLNKLKL-LRIS 454
Db 400 -----ALGGLGVSLASQALGSL-LGVTVAFAGLLVYGLMKALLGIRLSQ 444
QY 455 EDELAMDMTRHGGFAFAYE 474
Db 445 BEEYVGADLSHKIGATISHE 464

RESULT 8
US-09-134-001C-3907
; Sequence 3907, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3907
; LENGTH: 437
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3907

Query Match 15.4%; Score 406.5; DB 4; Length 437;
Best Local Similarity 26.0%; Pred. No. 7.7e-35;
Matches 118; Conservative 80; Mismatches 191; Indels 65; Gaps 13;

QY 48 DNTYLLFSAYLVFSQGLFAMLCAGSVRAKTNMILTNVLDAAAGLFPYLLFGFAFAG 107
Db 26 DTIFLFLCTLLVLMTPGLSLFYGLGVQSKALNTVMQSWAIVIVTFVMIIGFSLFD 85
QY 108 SPSN-----GFIGKHFFGLK-----DIPSSSYDSYFLYQWAFATAAGITSGIAER 155
Db 86 GGNQWIGGLKFLGLHVGFEITSKILSPHPLS-----LFMLFQMMFCTIAVSILSGSIAEK 141
QY 156 TQFVAVLIYSSFLTGFPYVWVSHWSPDGMASAFKITDRLFSTGVDFAGSGVYHMGV 215
Db 142 MRPIPYLIEVSLWVLLIYSPVAHWYWG--GGWIS-----KIGADYAGTGVVHITSG 191
QY 216 IAGLWCALLGEGPRMGRFDHAGRAVALRHGASLVVLGTFLWFGYNGPSPGSG---FNKIL 272
Db 192 VSLGLVIGIMIGIKKEXHT-----FNNLLITLIGLILWLGWYGNVGSATTFDHIA 244
QY 273 LTYGNSGNYQWSAVGRTAVTTTLAGSTAAITTLFGKRVISGHWNVDVNCNGLLGFAA 332
Db 245 MI-----SFVNTVIGASAGAFGWLIFEYILKKTLSLGLSLGSLGLVA 288
QY 333 ITAGCSVPEPAAIVCGFVASI-VLIACNKLAEKVKFDDPLEAAQLHGGCGTGWVIFTAL 391
Db 289 ITPAAGTVSYNMGAMIIATIGGCCIVINLIKVKLOYNDALDAFGIHGVGILGAVLTGV 348
QY 392 FAKKYEYKVEYGLGRAHGLLMGGGKLLAAHVIGILVIAGWVSATMGLPFWGLNKLKL-- 449
Db 349 FQSHQINSAV-----QNGFIYADPKV---VIQGAALATVVSATVTFIARFIKIFT 400
QY 450 -LRISSEDELAMDMTRHGGFAFAY-EDDETHKH 481

Db 401 PLATTOEDKGTGLDAIVHGEKAYFYGELNKENRH 434

RESULT 9

US-09-134-000C-5907

Sequence 5907, Application US/09134000C

Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/055,778

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SOFTWARE: PatentIn version 3.1

SEQ ID NO 5907

LENGTH: 361

TYPE: PRT

ORGANISM: Enterococcus faecalis

US-09-134-000C-5907

Query Match 7.7%; Score 203.5; DB 4; Length 361;

Best Local Similarity 20.5%; Pred. No. 3.6e-13;

Matches 75; Conservative 72; Mismatches 169; Indels 49; Gaps 10;

QY 47 VDNVTYLLFSAIYVFNQGLFAMLCAGSVRAKNTNMIMLTNLDAAAGLFYVYLFQPAFAF 106

Db 6 MNNLFVFCFPMWLMIFVILYVGLVNHRYHHTLILGIVTIISGLWLFVGYLSL- 64

QY 107 GPSNGFIQGHFGLKIDPSSSYDSYFYLQWAFIAAAGITSGIAERTOFVAYLIYSS 166

Db 65 -----FFGNIQVSYFISPLASSEIVSILQLLCLYSVIMIGSVILRGWKNKIVLFPV 118

QY 167 FLTGFPYVPUVSHWFSKPDGASAFKIDRLFTGTVIDRAGSVHVMVGGIAGLWGLIEG 226

Db 119 LWIVFVAPVCSLWGHGNW-----LGKIGVDSYSGGLVWHVHTAGISLVLAITS 169

QY 227 PRMGREDHAGRAVALRHGHSASIVV-LGTFLWFGYGNPQSFNKLITYGNSGNYGQW 285

Db 170 IRLKN-----SLIFKQEMIAFVGMFLITLWFGFNWAPSGKI-----GEE 210

QY 286 S-AVGRTAVTTTLAGSTAALTTLFGKRVISGHNWVTDVNCGLGGFAAITAGCSVVEP-- 342

Db 211 SIQIWLNTLISILGGS---ISWPFQWILIKKVSYSIMNGIIGELVGSTCSGYISPAI 267

QY 343 ---WAAIVCGFVASIVLIAACNKLAEKVKFDDPLEAAQLHGGCGGTWGVIFTFALPARK-EYV 398

Db 268 SLLISIVTCTCPVIVHMLRIA---NFDDAADSFGMNAVGGIAGSILTGWMAEKGDFF 324

QY 399 KEVYG 403

Db 325 LQLFG 329

RESULT 10

US-09-107-532A-3674

Sequence 3674, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Atinello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3674:

SEQUENCE CHARACTERISTICS:

LENGTH: 223 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORIGINAL SOURCE:

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (8) LOCATION 1...223

SEQUENCE DESCRIPTION: SEQ ID NO: 3674:

US-09-107-532A-3674

Query Match 7.3%; Score 193; DB 4; Length 223;

Best Local Similarity 26.9%; Pred. No. 2.3e-12;

Matches 60; Conservative 35; Mismatches 102; Indels 26; Gaps 4;

QY 242 RCHSASLV--VLGTFLLWFGYGNPQSFNKLITYGNSGNYGQWAVGRTAVTTTLG 299

Db 16 RSQSHSLMAAAIGTGLLWFGWFGNSGG---ALRADQAVNAFG-----STFIAL 62

QY 300 STAATLTTLFGKRVISGHNWVTDVNCGLGGFAAITAGCSVVEPAAIVCGFVASIVLIAC 359

Db 63 AFAMITWLIIAKVGNGEDFVDVLTGTVAGLAITPCAGYVEAKSAMLGIAGIVCHAA 122

QY 360 NKLAEKVKFDDPLEAAQLHGGCGGTWGVIFTFALFAKKEVYKVEYGLGRAHGLLMGGGKLL 419

Db 123 VDFRKKQWMDALDVGVHGMGFTGTILIGIFA-----SNSHLITNPSSWYFL 171

QY 420 AAHVITQILVIAGWVSATWGPLFWGLNKLKLLRISSEDELAGMD 462

Db 172 GIOVIGVITAVYAVVLTVTILKSAKHFTTITTYKBEQEGLD 214

RESULT 11

US-09-107-532A-4102

Sequence 4102, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD/ROM ISO9660
 COMPUTER: PC
 OPERATING SYSTEM: <Unknown>
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/107,532A
 FILING DATE: 30-Jun-1998
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/085,598
 FILING DATE: 14 May 1998
 APPLICATION NUMBER: 60/051571
 FILING DATE: July 2, 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Ariniello, Pamela Deneke
 REGISTRATION NUMBER: 40,489
 REFERENCE/DOCKET NUMBER: GTC-012
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (781)893-5007
 TELEFAX: (781)893-8277
 INFORMATION FOR SEQ ID NO: 4102:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 224 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHEICAL: YES
 ORIGINAL SOURCE:
 ORGANISM: Enterococcus faecium
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (B) LOCATION 1...224
 SEQUENCE DESCRIPTION: SEQ ID NO: 4102:

Query Match 6.9%; Score 182; DB 4; Length 224;
 Best Local Similarity 26.7%; Pred. No. 3.5e-11;
 Matches 52; Conservative 21; Mismatches 102; Indels 20; Gaps 4;

QY 48 DNTVLLSAVLPMSQGLGAMLCAGSVRAKNTWNIMLTNVLDAAGGLFYLLFGFAFAG 107
 DB 34 DTAEMILCTAMVCLNTGLAFFYGLARKNIIITMSQSLVSGITITWVFGGFLAFG 93
 QY 108 SPNSNGFTGK--HPFGLKDIPISSVDY-----SYFLYQWAPATAAGITSGIAERTQ 157
 DB 94 RDIGVIGNPADFLMRHTVSFFNMFGATIPFLMFLYQLMFIIVTPLMTGAFAGRLN 153
 QY 158 FVAVLYSSFLTGVPVVSFWSPDGMASAFKIDRLFTSGVIDFAGSGVVMVGGIA 217
 DB 154 LKGVIILVIFWNLIIYPPVCHWI-----WGCGF-----LDQMGFRDPAGAVIHITAGFG 203

RESULT 12
 US-09-489-039A-9335
 ; Sequence 9335, Application US/09489039A
 ; Patent No. 6610836

GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 9335
 LENGTH: 443
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae

US-09-489-039A-9335

Query Match 5.2%; Score 136; DB 4; Length 443;
 Best Local Similarity 22.4%; Pred. No. 8.9e-06;
 Matches 105; Conservative 55; Mismatches 162; Indels 146; Gaps 25;
 QY 57 YLVFSNQLGFAMLCAGSVRAKNTWNIMLTNV-----LDAAGGLFYLLFGFAFAGS-PS 110
 DB 17 YLILLM---IFVTVAVNYGDRATLSIAGTEVAKELGSAVSMGYIFSAFGVAILMQIPG 73
 QY 111 NGFIGKHFFGLKDIPISSVDYSYFLYQW-----FAIAAGITSGISAERTQV 159
 DB 74 GWLLOK--FGSKKV-----YSYSLFWSLFTFLQGGIDVFPLAWAGVS----- 114
 QY 160 AVLIYSSFLTGFP-----VVP-----VVSFWSPD-GWASAFKITDRLES-----TGVID 203
 DB 115 --MFTMRFMLGFSEAPSPANARIVAAMFPAKERTASAFNAAYFSLALFSPLLGLWT 172
 QY 204 FA-GSGVHMVGGIAG-----LWGALI-----EGPRMGR-----FDHAGRAV 239
 DB 173 FALGHEHVTWGLIGFVLITIVKVFHNPTDHRMSAELKYISEGGVVDMDHKEAT 232
 QY 240 ALRGHSASLV-----VLGTFLMFGWYGFNPGSFNKKILLTYGNSGNYGQW---SAV 288
 DB 233 PAAGPKMDYIROLITNRMLGVF---FGQYFLN-----TITW-----FFLTWFPYILV 277
 QY 289 GRTAVTTILAGSTAALTTLFGKRVISGHNVTVCNGLLGGFAA---ITAGCSVV-EPWA 344
 DB 278 QDKGMSILKGVFVASIPALFG-----FAGVGLGFLSDYLLIGRGTITLPARKL 325
 QY 345 AIVCGFVASIVLIACNKLAEKVKFDDPLAQAQLGGCGTGWIVTALFAKKEYTK----- 399
 DB 326 PIVLGMLLASSIILCNVTASTPLVITLMALAFGKGFALGWPVISDVAPKEIYGLCGGV 385
 QY 400 -EYVG-----LGRAHGLMGGGKLLAAHVIOILVI 429
 DB 386 FNVFGNVASIAIPLVIGYIVSELHSFNCGALIFVGGSALMMVMVCLFVV 433

RESULT 13

US-09-489-039A-9610
 ; Sequence 9610, Application US/09489039A
 ; Patent No. 6610836
 GENERAL INFORMATION:
 APPLICANT: Gary Breton et. al
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
 TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 2709.2004001
 CURRENT APPLICATION NUMBER: US/09/489,039A
 CURRENT FILING DATE: 2000-01-27
 PRIOR APPLICATION NUMBER: US 60/117,747
 PRIOR FILING DATE: 1999-01-29
 NUMBER OF SEQ ID NOS: 14342
 SEQ ID NO 9610
 LENGTH: 490
 TYPE: PRT
 ORGANISM: Klebsiella pneumoniae

Query Match 4.6%; Score 121.5; DB 4; Length 490;
 Best Local Similarity 19.4%; Pred. No. 0.00037;
 Matches 103; Conservative 61; Mismatches 134; Indels 233; Gaps 27;
 QY 13 QLLGPNNTDASAAASLICGHFAAVDSKFVDTAFA-----VDNTYLLF-----SAY 57
 DB 63 QMAGP---ALALVYLCGIF-----SFFILRALGELVLRHPPSSGFSVYAREFLGEKAY 114
 QY 58 LVFSMQLGFAMLCAGSVRAKNTWNIMLTNVLDAAGGLFYLLFGFAFAGSPSNGFIKXH 117
 DB 115 VAGWVYF-----VNWMTGIVDITVALYMYWG---AFG----- 146
 QY 118 FFGKIDPSSVDYSYFLYQWAFATAAGITSG-----SIAERTQFVAY 161

147 -----DVP-----QWPFALGALAIAGTMMNMGVKNFAEMEFNALVKVLAIVAF 190
162 LIYSSFLTGFPVYVWSHFWSPDGMASAK-ITDR--LFSTGVID-----FAGSGV 209
191 LVGTTFPLGSGKFL-----DGNATGPHLITDNGGFPFHLLPALVLVQGVVFPAS- 241
210 VHMVGGIAG-----LWGALIEBGRMGRFDHAGRAVALRGHSASLVVIGT 253
242 IELVGTAAAGCKDPEWPKAINSVIW-----RIGLF-----YVGSVLLVL 283
254 FLWFGHY-GFNP-----GS-FNKILTYG-----NSNGYQWMSAVGRTAVT 294
284 LLPWAIYQACQSPFTVFFSKLGVYVIGSVNIVLVLTAAALSSNSGLY-----STGRIIRS 338
295 TTLAGSTAALTTLFGKRVISGHNVTDVNGLLGGFAAITAGCSVVPEWAAIVCGFVASI 354
339 MSMGSAKPKFMSKMRHV-----PYAGLILATLGVVV 370
355 VLIACNKLAEKVDFDPLEAAQLHGGCGTWGVIPTALFAKKEVYKVEVYGLGSA-----407
371 VGFELNLYVPSQVFEIVLVNASL-GIIASGFIWVCOMRLRKAKE-----GKAAKVSPRM 425
408 -----HGLLMGGGKLLAAHVITQILVIAGW 432
426 PGAPFTSWLTTLFVSVLWAFDYPNGTYTIGSIPLA-----VLVAGW 471

RESULT 14
US-09-252-991A-19322
; Sequence 19322, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107:96.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19322
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19322

Query Match 4.5%; Score 119.5; DB 4; Length 517;
Best Local Similarity 22.3%; Pred. No. 0.00067;
Matches 107; Conservative 54; Mismatches 193; Indels 125; Gaps 24;
QY 14 LLGNPTDASAAASLICHFAAV--DSKFVDYAFADVNTYLL-FSAYL-VFSMQ-----63
DB 38 MAGNVHTSAALEIEGALCATPEEGSWISTAYLVASISWILPTAWLVEVSLRVMLL 97
QY 64 --LGFAMLCAGSVAKNTMIMLVNLDAAAGGLFYVLFQFAFGSPNGFIKHFGL 121
DB 98 GSVLFLSSLSLSCALAPNLSTILIRVIQAGSAGVLIPL-----SNQLI-----L 141
QY 122 XDIPSSSYDYSELYQWAFATA-AAGITSGSIAERTQFVAYLIYSSFLTGFPVYVSWHF 180
DB 142 TELPSSRIPLGNALFUSNSVAQAGSFGWLDAYSWEIFLQLLPGIALLAAVMS 201
QY 181 WSP-DGNASAFKITDRLFSTGVIDFAGSVVHVGGIAGLWALIEGPRMGRFDHAG-RA 238
DB 202 IRPRDGRRLRQADWL-----GICAMVAGLQIVLEEGGRDWPESGFIRT 250
QY 239 VALRGHSASLVVIGTFL-----LM-----FGMYGFNPGSFNKILLITYGNSG----279
DB 251 FAV-----LAVLALLFPVQLMGARPFINLRLLGSYFNFGVSSLAMAVFGAATFGLVFL 304

QY 280 --NYTQWMSAVGRTAV--TTTLAGSTAALTTLFGKRVISGHNVTDVNGLLGGFAAITA 335
DB 305 VPNYLSQLQGPNARQIGDSILYGLVQLLAPLPLRLM--RMLNPKLL--VAGGFAMAL 360
QY 336 GC-----SWPEPWAIVCGFVASIVLTACNKLAEKVDFDPLEAA-----375
DB 361 GCMWGHMLNADAGRNIIP-SIVVRGIGQPLIMWALSILA--VKGLDKAEAGSASALISM 417
QY 376 --QLHGGCGTWGVIPTALFAKKEVYKVEVYGLGRAHGLMG-----GGGKL 418
DB 418 LRNLGGAIGT--ALLTQVLSRE-----RFSHERIGETLTIFDGLAQOORLGGGV 465
RESULT 15
US-09-252-991A-18216
; Sequence 18216, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107:96.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18216
; LENGTH: 557
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18216

Query Match 4.5%; Score 119; DB 4; Length 557;
Best Local Similarity 24.0%; Pred. No. 0.00085;
Matches 85; Conservative 34; Mismatches 109; Indels 126; Gaps 19;
QY 164 YSSFLTGFPVYVWSHFWSPDGMASAFKITDRLFSTGVIDFAGSVVHVGGIAGLWAL 223
DB 54 YDFLYGALAAVISKQFFAGVNDTAFALMAFAAGF-----LVRFPGAL 99
QY 224 IEGPRMGRFDHAGR-----AVALRGHSASLVVLTGTFLLNFGWYGNP-----GSFNKIL 272
DB 100 VFG-RMG--DMIGRKYTFVLTLIMG-----LSTFAV-----GLLPTYASIGVAAPII 144
QY 273 LT-----YGNNGNYGOWSAVGRTAVTTLTAGSTAALTTLFGKRVISGHNVT 319
DB 145 LVTRMLQGLGGEYGGAAIYVAEHAPANKGYSYTSWISTATLGLLLSLVIL-----199
QY 320 TDVNGLLGGAFAITAGCSVVEPWAIVCGFVASIVLIACN-----KLAE-----KVXFD 369
DB 200 --ACRQLTG-----DEFETGWRL--PFLLSIVLLGISTWIRLSMRSPAPFKMAE 247
QY 370 DPLEAQLHGGCGTWG--VIFTALF-----AKKEYKVEVYGL-----GRAHG 409
DB 248 GKYSKAPLRESFTQWNLKVLTALFESINAGQVTFYTAQFVLFVLTQVLKVDGTANG 307
QY 410 LLMGGGGKLLAAHVI--QILVITAGWVSATWG-----PLFWGL 444
DB 308 L-----LIVALVLGAPFFIVAGMLSDRIGRPVLLAGLLLATLIFYPFLFKGL 354

Search completed: March 9, 2004, 11:56:43
Job time : 24 secs

GenCore version 5.1.6
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DM protein - protein search, using sw model

Run on: March 9, 2004, 11:55:40 ; Search time 39 Seconds
(without alignments)

2707.093 Million cell updates/sec

Title: US-10-033-109-4

Perfect score: 2639

Sequence: 1 MSLPACPAEQALQLGNTT.....HGMQLRRVGNASSPTTDE 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21113259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pcp.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pcp.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pcp.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pcp.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pcp.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pcp.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pcp.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pcp.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pcp.*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pcp.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pcp.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pcp.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pcp.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2639	100.0	500	13	US-10-033-109-4
2	2129.5	80.7	501	8	Sequence 4, Appli
3	1954	74.0	494	13	Sequence 2, Appli
4	775	29.4	459	9	Sequence 6, Appli
5	775	29.4	459	14	Sequence 32, Appl
6	775	29.4	459	14	Sequence 32, Appl
7	707.5	26.8	395	15	Sequence 32, Appl
8	707.5	26.8	395	15	Sequence 100, App
9	677.5	25.7	373	15	Sequence 100, App
10	613	23.2	183	13	Sequence 250, App
11	535	20.3	436	14	Sequence 2, Appli
12	483	18.3	446	14	Sequence 13126, A
13	449.5	17.0	492	9	Sequence 10188, A
14	430.5	16.3	438	9	Sequence 192, App
15	414	15.7	499	9	Sequence 6981, Ap
					Sequence 194, App

16	363.5	13.8	452	9	US-09-738-626-6968	Sequence 6968, Ap
17	335.5	12.7	470	13	US-10-033-109-14	Sequence 14, Appl
18	327.5	12.4	486	13	US-10-033-109-12	Sequence 12, Appl
19	314	11.9	497	13	US-10-033-109-10	Sequence 10, Appl
20	180	6.8	458	15	US-10-190-115-59	Sequence 59, Appl
21	180	6.8	458	15	US-10-369-072-59	Sequence 59, Appl
22	173.5	6.6	458	15	US-10-190-115-55	Sequence 55, Appl
23	173.5	6.6	458	15	US-10-190-115-56	Sequence 56, Appl
24	173.5	6.6	458	15	US-10-369-072-55	Sequence 55, Appl
25	173.5	6.6	458	15	US-10-369-072-56	Sequence 56, Appl
26	165	6.3	488	15	US-10-074-978A-248	Sequence 248, App
27	158	6.0	458	15	US-10-190-115-57	Sequence 57, Appl
28	158	6.0	458	15	US-10-369-072-57	Sequence 57, Appl
29	157	5.9	467	15	US-10-074-978A-247	Sequence 247, App
30	151	5.7	498	9	US-09-949-145-4	Sequence 4, Appli
31	151	5.7	498	15	US-10-074-978A-245	Sequence 245, App
32	148	5.6	455	15	US-10-190-115-58	Sequence 58, Appl
33	148	5.6	455	15	US-10-369-072-58	Sequence 58, Appl
34	147	5.6	459	15	US-10-074-978A-246	Sequence 246, App
35	139	5.3	479	9	US-09-949-145-3	Sequence 3, Appli
36	139	5.3	479	15	US-10-074-978A-244	Sequence 244, App
37	134	5.1	431	15	US-10-369-493-13974	Sequence 13974, A
38	132	5.0	432	15	US-10-369-493-15510	Sequence 15510, A
39	132	5.0	432	15	US-10-369-493-15882	Sequence 15882, A
40	132	5.0	432	15	US-10-369-493-16254	Sequence 16254, A
41	131.5	5.0	388	15	US-10-074-978A-249	Sequence 249, App
42	131.5	5.0	445	15	US-10-074-978A-42	Sequence 42, Appl
43	131.5	5.0	448	15	US-10-190-115-22	Sequence 22, Appl
44	131.5	5.0	448	15	US-10-369-072-22	Sequence 22, Appl
45	130.5	4.9	326	15	US-10-264-237-2412	Sequence 2412, Ap

ALIGNMENTS

RESULT 1

US-10-033-109-4
; Sequence 4, Application US/10033109
; Publication No. US20020142390A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/10/033,109
; CURRENT FILING DATE: 2001-12-28
; PRIOR FILING DATE: EARLIER FILING DATE: 09/384,625
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
; PRIOR FILING DATE: EARLIER FILING DATE: 60/098,248
; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 500
; TYPE: PRT
; ORGANISM: Glycine max

Query Match	100.0%	Score	2639	DB	13	Length	500
Best Local Similarity	100.0%	Pred. No.	6.7e-256				
Mismatches	500	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	MSLPACPAEQALQLGNTT	DASAAALICGHFAVDKSFVDTAFAVNTVLLFSAYLVF	60			
Db	1	MSLPACPAEQALQLGNTT	DASAAALICGHFAVDKSFVDTAFAVNTVLLFSAYLVF	60			
Qy	61	SMQLGFAMLCAGSVRAKNTN	IMLNTVLDAAAGGLFYLLFGFAFGSPNGFIKGFPG	120			
Db	61	SMQLGFAMLCAGSVRAKNTN	IMLNTVLDAAAGGLFYLLFGFAFGSPNGFIKGFPG	120			
Qy	121	LKQIPSSVDYSYFLYQWAF	ATAAAGITSGTAETQFVAILYSSFLTGVPYVWSHF	180			
Db	121	LKQIPSSVDYSYFLYQWAF	ATAAAGITSGTAETQFVAILYSSFLTGVPYVWSHF	180			

121 LKDIPISSYDYSLFYQWAFALAAAGITSGIAERTQFVAYLIYSSFTGFVYVWHSWF 180
181 WSPDGWASAFKIDTRLFSTGVDFAGSGVWVHVGIGALWGALIEGPMGRFDHAGRAVA 240
181 WSPDGWASAFKIDTRLFSTGVDFAGSGVWVHVGIGALWGALIEGPMGRFDHAGRAVA 240
241 LRHSASLVVLGFTFLWFGWGFNPGSFNKLITTYGNSGNYGQMSAVGRVAVTTTLAGS 300
241 LRHSASLVVLGFTFLWFGWGFNPGSFNKLITTYGNSGNYGQMSAVGRVAVTTTLAGS 300
301 TAALTTLFGKRVISGHWNTDVCNGLLGGFAAITAGCSVVEPWAAIVCGFVASIVLIACN 360
301 TAALTTLFGKRVISGHWNTDVCNGLLGGFAAITAGCSVVEPWAAIVCGFVASIVLIACN 360
361 KLAEKVKFDDPLEAAQLHGGCGTGWGVIPTALPAKKEVYKVEVYGLGRAHGLLGGGKLLA 420
361 KLAEKVKFDDPLEAAQLHGGCGTGWGVIPTALPAKKEVYKVEVYGLGRAHGLLGGGKLLA 420
421 ARVITQIIVAGWSATWGPFLFWGLNKLKLLRISSDELAGMDTRHGGFAVAYEDDETHK 480
421 ARVITQIIVAGWSATWGPFLFWGLNKLKLLRISSDELAGMDTRHGGFAVAYEDDETHK 480
481 HGMQLRRVGNASSTPTTDE 500
481 HGMQLRRVGNASSTPTTDE 500

RESULT 2
JS-08-635-967-2
; Sequence 2, Application US/08635967
; Publication No. US2001003848A1
; GENERAL INFORMATION:
; APPLICANT: FROMMER, Wolf-Bernd
; APPLICANT: NINEMAN, Olaf
; TITLE OF INVENTION: DNA SEQUENCES FOR AMMONIUM TRANSPORTER,
; TITLE OF INVENTION: PLASMIDS, BACTERIA, YEASTS, PLANT CELLS AND PLANTS
; TITLE OF INVENTION: CONTAINING THE TRANSPORTER
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ostrolenk, Faber, Gerb & Soffen, LLP
; STREET: 1180 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10036-8403
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,967
; FILING DATE: 29-APR-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP 94/03499
; FILING DATE: 24-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 43 37 597.9
; FILING DATE: 28-OCT-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weilman, Edward
; REGISTRATION NUMBER: 24,735
; REFERENCE/DOCKET NUMBER: P/951-120
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 382-0700
; TELEFAX: (212) 382-0888
; TELEX: 236925
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 501 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-635-967-2
Query Match 80.7%; Score 2129.5; DB 8; Length 501;
Best Local Similarity 80.9%; Pred. No. 9.1e-205;
Matches 407; Conservative 42; Mismatches 39; Indels 15; Gaps 7;
QY 5 ACPABQLAQLGPNVTTDASAAALICGHFAAVDSKFVDTAFAVDNTVLLPSAYLVFSMQL 64
DB 2 SCSATDLAVLLGPN---ATAAAAYICQGLGVDNKFIDTAFADNTVLLPSAYLVFSMQL 58
QY 65 GFAMLCAGSVRAKNTMIMLTNVLDAAGGLFYFLFGFAFGSPSNGFIKHFGLKDI 124
DB 59 GFAMLCAGSVRAKNTMIMLTNVLDAAGGLFYFLFGFAFGSPSNGFIKHFGLKDI 118
QY 125 PSSYDYSLFYQWAFALAAAGITSGIAERTQFVAYLIYSSFTGFVYVWHSWFSPD 184
DB 119 PTASADYSLFYQWAFALAAAGITSGIAERTQFVAYLIYSSFTGFVYVWHSWFSPD 178
QY 185 GWASAFKIT-DRLFSFTGVDFAGSGVWVHVGIGALWGALIEGPMGRFDHAGRAVALRG 243
DB 179 GWASAFKITDGLLFFSTGAIDFAGSGVWVHVGIGALWGALIEGPMGRFDHAGRAVALRG 238
QY 244 HSASLVVLGFTFLWFGWGFNPGSFNKLITTYGNSGNYGQMSAVGRVAVTTTLAGSTAA 303
DB 239 HSASLVVLGFTFLWFGWGFNPGSFNKLITTYGNSGNYGQMSAVGRVAVTTTLAGSTAA 297
QY 304 LTLFGKRVISGHWNTDVCNGLLGGFAAITAGCSVVEPWAAIVCGFVASIVLIACNKL 363
DB 298 LTLFGKRLLSGHWNTDVCNGLLGGFAAITAGCSVVEPWAAIVCGFVASIVLIACNKL 357
QY 364 EKVKFDPLEAAQLHGGCGTGWGVIPTALPAKKEVYKVEVYGLGRAHGLLGGGKLLA 421
DB 358 EKLKYDDPLEAAQLHGGCGTGWGVIPTALPAKKEVYKVEVYGLGRAHGLLGGGKLLA 417
QY 422 HVTQIIVAGWSATWGPFLFWGLNKLKLLRISSDELAGMDTRHGGFAVAYEDDETHK 480
DB 418 QLIQIIVAGWSATWGPFLFWGLNKLKLLRISSDELAGMDTRHGGFAVAYEDDETHK 477
QY 481 HGMQLRRVGNASSTPTTDE 497
DB 478 -AQLRRVGNASSTPTTDE 499

RESULT 3
US-10-033-109-6
; Sequence 6, Application US/10033109
; Publication No. US20020142390A1
; GENERAL INFORMATION:
; APPLICANT: Allen, Stephen M.
; APPLICANT: Rafalski, J. Antoni
; APPLICANT: Sakai, Hajime
; TITLE OF INVENTION: Nitrogen Transport Metabolism
; FILE REFERENCE: BB-1210
; CURRENT APPLICATION NUMBER: US/10/033,109
; PRIOR FILING DATE: 2001-12-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/384,625
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/098,248
; PRIOR FILING DATE: EARLIER FILING DATE: 28 August 1998
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 6
; LENGTH: 494
; TYPE: PRT
; ORGANISM: Triticum aestivum
; US-10-033-109-6
Query Match 74.0%; Score 1954; DB 13; Length 494;
Best Local Similarity 74.8%; Pred. No. 3.6e-187;
Matches 374; Conservative 46; Mismatches 62; Indels 18; Gaps 5;
QY 3 LPACPAQLAQLGPNVTTDASAAALICGHFAAVDSKFVDTAFAVDNTVLLPSAYLVFSM 62

1 MSATCAADLGPLIG---AAAANATDVLNRFPA-----DITSAVDSTVLLFSAYLVFAM 50
63 QLFAMLCAGSVRAKNTMIMLTNVLDAAGGLFYVLGFAFAPGSPNGTIGKHFGLK 122
51 QLFAMLCAGSVRAKNTMIMLTNVLDAAGALFYVLGFAFAPGSPNGTIGKHFGLK 110
123 DIPSSYDYSFLYQWAFIAAAGITSGSIABRTQFVAYLYSSFLTGFPVVPVSHNFW 182
111 DMPQTGDFYSFELFQWAFIAAAGITSGSIABRTQFVAYLYSSFLTGFPVVPVSHN 170
183 PDQWASAFKIT-DRLFTSTGVIDPAGSVVHMVGGTAGLWALIEGPRMRDTHAGRAVAL 241
171 VDGWASAAATSGPLPKSGVIDPAGSVVHMVGGTAGLWALIEGPRMRDTHAGRSVAL 230
242 RGHASLVVLGTFLLWFGWYGFNPGSFNKILLTYGNSGNYQWQSAVGRVATVTTLAGST 301
231 KGHASLVVLGTFLLWFGWYGFNPGSFVILKSYGPPGSGINGQWGVGRTAVTTLAGSV 290
302 AALTTLFGKRVISGHWNVTVCNGLLGGFAATAGCSVVEPWAATVCGFVASIVLIACNK 361
291 AALTTLFGKELQTHWNVVDVCNGLLGGFAATAGCSVVDPAWAVICGFVSANWLLIGLNA 350
362 LAEKVFEDEPLEAAQLHGGCGTGWVIFTALFAKKEYVKEVYGLGRAHGLLGGGKILAA 421
351 LAGLKVDDPLEAAQLHGGCGANGIIFTALFAKQVVEIYAGRPYGLFLGGGRLLAA 410
422 HVQILVIAGVWATWGLPFWGLNKLRLRISSEDELAGMDWTRHGGFAYVEDDETHKH 481
411 HIVQILVIAGVWATWGLPFWGLNKLRLRISAEDEMAWMDLTRHGGFAYVYHDDDEHK 470
482 ---GMQLR---RVGNASS 494
471 SVGGFMLRSQTRVEPAAA 490

RESULT 4
US-09-795-693-32
; Sequence 32, Application US/09795693
; Patent No. US20020068710A1
; GENERAL INFORMATION:
; APPLICANT: Gluckmann, Maria A.
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33894, and
; FILE OF INVENTION: 32613, No. US20020068710A1el Human Transporters
; FILE REFERENCE: 35800/209292
; CURRENT APPLICATION NUMBER: US/09795,693
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pfam consensus sequence
US-09-795-693-32

Query Match 29.4%; Score 775; DB 9; Length 459;
Best Local Similarity 41.3%; Pred. No. 6.8e-69;
Matches 191; Conservative 60; Mismatches 162; Indels 50; Gaps 17;
QY 52 LLFSAYLVFSMQLGFAMLCAGSVRAKNTM--IMLTNVLDAAG--GLFYVLGFAFAP-- 106
DB 4 LISAALVIFWMPQGFALLIESGLVRSKNVLFILKNFVDLAIGICVLYAYVLFYSLAFGD 63
QY 107 --GSPNSGFIKHFH-----GLKD--IPSSSYDYSVFLYQWAFI--AAAGITS 149
DB 64 SYGEPGNGFINGLWVLPKFLGVSAGIQQDTLPDQ---LPFFLQLMFAKTAATIIIS 120
QY 150 GSIAERTQFVAYLYSSFLTGFPVVPVSHNFWSP--DGWASAFKITDRLFTSTGVIDFAGS 207

121 GAVABRIKFSAYLLFSALLGTLVYPPVAHWNWGLVGNWLAQLGVLLVILKTKAIDFAGS 180
208 GYVHMVGGTAGLWALIEGPRMRFP--DHAGRAVALRGHSASLVVLGTFLLWFGWYGNP 265
181 TVHIVGGVAGLAALVILGPRIGRPDDTCKPEAIRPHNLPPFAVLGTFLLWFGWFGFNA 240
266 GSFNKILLTYGNSGNYQWQSAVGRVATVTTLAGSTAAITLFGKRVISGHWNVTVCNG 325
241 GS---ALTANGRAAAGAGWSTVARAAVNTLAAAGALTWLLISRLKTKGPTVVLGLANG 297
326 LGGGFAAI--TAGCSVVEPWAATVCGFVASIVLI-----ACNKLAEKVFDPLLEAAQLHG 379
298 ALAGLVAICTPACGVVSPWALIIGLVAGVLSVLGVKYLTPKLEKLGIDDPDLPVFPVHG 357
380 GCGTGWVIFTALFAKKEY-----VKEVYGL---GRAHGLLGGGG--KLLAAKVIQILVIAG 431
358 VGGIMGGIAGVIFAAPKPNYNNIGFPPEYGAISTSGISGGLLYGNGGFKQLGVQLIGIAVILA 417
432 W---VSATMGPLFWGLNKLRLRISSEDELAGMDWTRHGGFAY 471
418 YAGVTFILAKLL--GLTGGKLRVSEEBEKVGLDLAEHGETAY 459

RESULT 5
US-10-156-239-32
; Sequence 32, Application US/10156239
; Publication No. US20030036074A1
; GENERAL INFORMATION:
; APPLICANT: Gluckmann, Maria A.
; TITLE OF INVENTION: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: Atpase Molecule, A Human Ubiquitin Hydrolase-Like Molecule, A H
; FILE OF INVENTION: Ubiquitin Conjugating Enzyme-Like Molecule, and Uses Therefor
; FILE REFERENCE: 35800/247645
; CURRENT APPLICATION NUMBER: US/10/156,239
; CURRENT FILING DATE: 2002-05-24
; PRIOR APPLICATION NUMBER: 09/795,693
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/185,906
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 09/809,557
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/192,018
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,568
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/191,790
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: 09/808,767
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 60/191,781
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pfam consensus sequence
US-10-156-239-32

Query Match 29.4%; Score 775; DB 14; Length 459;
Best Local Similarity 41.3%; Pred. No. 6.8e-69;
Matches 191; Conservative 60; Mismatches 162; Indels 50; Gaps 17;
QY 52 LLFSAYLVFSMQLGFAMLCAGSVRAKNTM--IMLTNVLDAAG--GLFYVLGFAFAP-- 106
DB 4 LISAALVIFWMPQGFALLIESGLVRSKNVLFILKNFVDLAIGICVLYAYVLFYSLAFGD 63
QY 107 --GSPNSGFIKHFH-----GLKD--IPSSSYDYSVFLYQWAFI--AAAGITS 149
DB 64 SYGEPGNGFINGLWVLPKFLGVSAGIQQDTLPDQ---LPFFLQLMFAKTAATIIIS 120

150 GSAERTQFVAVLIYSSFLTGFTVPVSHWSP--DQWASAFKITDLRSTGVIDRAGS 207
121 GAVARIKFSAYLLFSAIIGTLVTPVVAHWVWGVWGLAKGLVLLIKTKAIDFAGS 180
208 GVHVMVGGIAGLWALIEGPRMGRF--DHAGRAVALRHSASLVVLGTFLLWFGWYGFNP 265
181 TVHIVGVVAGLAALVLPGRIGRPDDTGKPEAIRPNLPPFAVLGTFLLWFGWGFNA 240
266 GSNFKILLTYGNSGNTYQWSAVGRTAVTTTLAGSTAATTLFGKRVISGHNWYDVCNG 325
241 GS---ALTANGRAAAAGAGSTVARAAVNTNLAAGALTWLLISRLTKGPTVLGLANG 297
326 LLGGFAAI--TAGCSVVEPAAI--VCGFVASIVLI-----ACNKLAEKVKFDDEPLEAAQLHG 379
298 ALAGLVAIGTACGVSPWAGALIIGLVAGVLSVGVKYLTPKLEKLGIDDDPLDVPFVHG 357
380 GCGTWGVIFTFALFAKKEY-----VKEVYGL---GRAHGLLMGGG-KLLAAHVLIQILVIAG 431
358 VGGIAGIAGVIFAAPKVNINIGFPPEYGAISTGIGGLLYGNGGFKOLGVLIGIAVILA 417
432 W---VSATMGPLFWGLNKLKLLRISSDELAGMDMTRHGGFAY 471
418 YAFGVTFILAKLL-GLTLGGKLRVSEEEKVGLDLAEHGETAY 459

RESULT 6
US-10-199-485-32
; Sequence 32, Application US/10199485
; Publication No. US20030077626A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria A.
; TITLE OF INVENTION: 20685, 579, 17114, 23821, 33834, and
; FILE REFERENCE: 32613, No. US20030077626A1el Human Transporters
; CURRENT APPLICATION NUMBER: US/10/199,485
; PRIOR FILING DATE: 2002-07-18
; PRIOR FILING DATE: 2001-02-28
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pfam consensus sequence
US-10-199-485-32

Query Match 29.4%; Score 775; DB 14; Length 459;
Best Local Similarity 41.3%; Pred. No. 6.8e-69;
Matches 191; Conservative 60; Mismatches 162; Indels 50; Gaps 17;

52 LIFSAYLVFMSQGLFAMLCAGSVAKNTMN-IMLTNVLDAAG--GLFYVLFQFAFAP-- 106
4 LISAALVIFMWQPGFALLESGLVSKVNFILMKNFVDLAIGICVLYVLFYGLAFGD 63
107 --GSPSNGFVIGKHPF-----CLKD--IPSSSYDYSLYLCWAPAI--AAAGITS 149
64 SYGEPGNGFIGNGLVWLFKFLGVSAGIQDGTUPDG---LPFFLQPMFAKTAATIIIS 120
150 GSAERTQFVAVLIYSSFLTGFTVPVSHWSP--DQWASAFKITDLRSTGVIDFAGS 207
121 GAVARIKFSAYLLFSAIIGTLVTPVVAHWVWGVWGLAKGLVLLIKTKAIDFAGS 180
208 GVHVMVGGIAGLWALIEGPRMGRF--DHAGRAVALRHSASLVVLGTFLLWFGWYGFNP 265
181 TVHIVGVVAGLAALVLPGRIGRPDDTGKPEAIRPNLPPFAVLGTFLLWFGWGFNA 240
266 GSNFKILLTYGNSGNTYQWSAVGRTAVTTTLAGSTAATTLFGKRVISGHNWYDVCNG 325

241 GS---ALTANGRAAAAGAGSTVARAAVNTNLAAGALTWLLISRLTKGPTVLGLANG 297
326 LLGGFAAI--TAGCSVVEPAAI--VCGFVASIVLI-----ACNKLAEKVKFDDEPLEAAQLHG 379
298 ALAGLVAIGTACGVSPWAGALIIGLVAGVLSVGVKYLTPKLEKLGIDDDPLDVPFVHG 357
380 GCGTWGVIFTFALFAKKEY-----VKEVYGL---GRAHGLLMGGG-KLLAAHVLIQILVIAG 431
358 VGGIAGIAGVIFAAPKVNINIGFPPEYGAISTGIGGLLYGNGGFKOLGVLIGIAVILA 417
432 W---VSATMGPLFWGLNKLKLLRISSDELAGMDMTRHGGFAY 471
418 YAFGVTFILAKLL-GLTLGGKLRVSEEEKVGLDLAEHGETAY 459

RESULT 7
US-10-190-115-100
; Sequence 100, Application US/10190115
; Publication No. US20030207394A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, John P. II
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Casman, Stacie J.
; APPLICANT: Grose, William M.
; APPLICANT: Gusev, Vladimir Y.
; APPLICANT: Ji, Weizhen
; APPLICANT: Lepley, Denise M.
; APPLICANT: Liu, Xiaohong
; APPLICANT: Mezick, Amanda J.
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Patturajan, Meera
; APPLICANT: Rastelli, Luca
; APPLICANT: Shen, Lei
; APPLICANT: Shency, Suresh G.
; APPLICANT: Shimkets, Richard A.
; APPLICANT: Spaderna, Steven K.
; APPLICANT: Spytek, Kimberly A.
; APPLICANT: Szekeres, Edward S. Jr.
; APPLICANT: Taupier, Raymond J. Jr.
; APPLICANT: Tchernev, Velizar T.
; APPLICANT: Zernhusen, Bryan D.
; APPLICANT: Voss, Edward Z.
; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
; FILE REFERENCE: 21402-050 CIP
; CURRENT APPLICATION NUMBER: US/10/190,115
; CURRENT FILING DATE: 2003-02-10
; PRIOR FILING DATE: 2003-02-10
; PRIOR FILING DATE: 2001-07-05
; PRIOR FILING DATE: 2002-04-01
; PRIOR FILING DATE: 2002-06-07
; PRIOR FILING DATE: 2002-06-07
; PRIOR FILING DATE: 2002-06-07
; PRIOR FILING DATE: 2000-07-03
; PRIOR FILING DATE: 2000-07-03
; PRIOR FILING DATE: 2000-07-03
; PRIOR FILING DATE: 2000-07-03
; PRIOR FILING DATE: 2000-07-03
; PRIOR FILING DATE: 2000-07-03
; PRIOR FILING DATE: 2001-07-07
; PRIOR FILING DATE: 2001-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-17
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: Curaseq version 0.1
; SEQ ID NO 100
; LENGTH: 395

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-190-115-100

Query Match      26.8%; Score 707.5; DB 15; Length 395;
Best Local Similarity 39.4%; Pred. No. 3.3e-62;
Matches 172; Conservative 60; Mismatches 147; Indels 57; Gaps 12;

QY 51 YLLFSAYLVSMQGFAMLCAGSVRAKNTNMIMTLNVLDAAAGGLFYVLFQFAPAFG-SP 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 WILISAALVIFMQFGFALLEGLVRSKNVNLNLYKQFQDVAIGVAYWGFYSLAFGKSY 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 110 SNGFIGKHFFGL-----KDIPSSYDYSYFLYQWAFALAAAGITSGIAERTQFVAYL 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 PSFGIGN--LGLLAAGIQWGTLP-----DGLFFFLQLMFAATAITIIISGAVARIKFSAYL 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 163 IYSSFLTGFPVYVSHWFPDQWASAFKITDRLFTSTGVIDFAGSVVHMVGGIAGLWGA 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 116 LFSALLGTLVYPPVAHVWVGEGWGLKGV-----LVDFAGSTVWHIFGQYAGLAAA 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 223 LIEGPRMGREDHAGRAVALRGHSASLVLTGTELLWFGWYGFNPGSFNKILLTYGNSGNY 282
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 LVLPGLRGFT---KNEAITPHNLPFAMLTGLLLWFGWGFNAGS-----209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 283 QGWSAVGR---TAVTTTLAGSTAALTTLFGKRVISGHNWVTVCGNLLGCFAPAITAGCSV 339
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 210 -ALAADGRARAAAVNTNLAAGGALTAILISRLKTGKPNMGLANGALAGLVAITPACGV 268
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 340 VEPWAAIVCGFVASIVLIACNK-LAEKVKFDDPLEAAQLHGCGGTGWTGIFTALFAKKEYV 398
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 269 VSPGALIIGLIGLVSLVGYKFKELGIDDDLDVFPVHVGVGGIAGVIFA-----323
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 399 KEVYGLGRAHGLMGGGKLLAAHVIOILVIAGW---VSATMGPLFWGLNKLKLRISSSE 455
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 324 -ALYVTSIGSGLLYGNKQGLGVQLIGIAVILAYAFGVTFILGL---LGLTLGLRVSEE 379
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

456 DELAGMDMTRHGGFAY 471
380 EEKVLDAVREHGETAY 395

RESULT 8
US-10-369-072-100
; Sequence 100, Application US/10369072
; Publication No. US20040014081A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P
; APPLICANT: Spaderna, Stephen K
; APPLICANT: Tchernev, Velizar
; APPLICANT: Liu, Xiaohong
; APPLICANT: Shenoy, Suresh
; APPLICANT: Spytek, Kimberly
; APPLICANT: Zethusen, Bryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Taupier, Raymond T
; APPLICANT: Rastelli, Luca
; APPLICANT: Grosse, William M
; APPLICANT: Szerkerez, Edward S
; APPLICANT: Lepley, Denise M
; APPLICANT: Shen, Lei
; APPLICANT: Burgess, Catherine E
; APPLICANT: Shimkets, Richard
; APPLICANT: Padigar, Muralidhara
; TITLE OF INVENTION: No. US20040014081A1el Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-050 CON2
; CURRENT APPLICATION NUMBER: US/10/369,072
; CURRENT FILING DATE: 2003-02-18
; PRIOR FILING DATE: 2002-06-17
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/898,994
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: 60/215,854
; PRIOR FILING DATE: 2000-07-03
```

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; PRIOR APPLICATION NUMBER: 60/215,856
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/215,902
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 60/216,585
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,586
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/216,722
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,622
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 60/218,992
; PRIOR FILING DATE: 2000-07-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 100
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Domain search
; OTHER INFORMATION: result
US-10-369-072-100

Query Match      26.8%; Score 707.5; DB 15; Length 395;
Best Local Similarity 39.4%; Pred. No. 3.3e-62;
Matches 172; Conservative 60; Mismatches 147; Indels 57; Gaps 12;

QY 51 YLLFSAYLVSMQGFAMLCAGSVRAKNTNMIMTLNVLDAAAGGLFYVLFQFAPAFG-SP 109
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 2 WILISAALVIFMQFGFALLEGLVRSKNVNLNLYKQFQDVAIGVAYWGFYSLAFGKSY 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 110 SNGFIGKHFFGL-----KDIPSSYDYSYFLYQWAFALAAAGITSGIAERTQFVAYL 162
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 62 PSFGIGN--LGLLAAGIQWGTLP-----DGLFFFLQLMFAATAITIIISGAVARIKFSAYL 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 163 IYSSFLTGFPVYVSHWFPDQWASAFKITDRLFTSTGVIDFAGSVVHMVGGIAGLWGA 222
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 116 LFSALLGTLVYPPVAHVWVGEGWGLKGV-----LVDFAGSTVWHIFGQYAGLAAA 167
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 223 LIEGPRMGREDHAGRAVALRGHSASLVLTGTELLWFGWYGFNPGSFNKILLTYGNSGNY 282
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 168 LVLPGLRGFT---KNEAITPHNLPFAMLTGLLLWFGWGFNAGS-----209
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 283 QGWSAVGR---TAVTTTLAGSTAALTTLFGKRVISGHNWVTVCGNLLGCFAPAITAGCSV 339
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 210 -ALAADGRARAAAVNTNLAAGGALTAILISRLKTGKPNMGLANGALAGLVAITPACGV 268
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 340 VEPWAAIVCGFVASIVLIACNK-LAEKVKFDDPLEAAQLHGCGGTGWTGIFTALFAKKEYV 398
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 269 VSPGALIIGLIGLVSLVGYKFKELGIDDDLDVFPVHVGVGGIAGVIFA-----323
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 399 KEVYGLGRAHGLMGGGKLLAAHVIOILVIAGW---VSATMGPLFWGLNKLKLRISSSE 455
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 324 -ALYVTSIGSGLLYGNKQGLGVQLIGIAVILAYAFGVTFILGL---LGLTLGLRVSEE 379
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

456 DELAGMDMTRHGGFAY 471
380 EEKVLDAVREHGETAY 395

RESULT 9
US-10-074-978A-250
; Sequence 250, Application US/10074978A
; Publication No. US20040010119A1
; GENERAL INFORMATION:
; APPLICANT: Leite, Mario
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Guo, Xiaojia (Sasha)
; APPLICANT: Fernandes, Elma
; APPLICANT: Li, Li
```


Query Match	25.7%; Score 677.5; DB 15; Length 373;
Best Local Similarity	40.1%; Pred. No. 3.1e-59;
Matches 167; Conservative 53; Mismatches 137; Indels 59; Gaps 14;	
QY	72 GSRAKNTMTMLTNLDAAGGLFYYLFQFAFG-SPSNGFIKHFFGI-----KD 123
Db	1 GLVRSEKNVILNYKDFDVAIGLVAYWGFYSIAPGDSYFSFGIN--LGLLAAGIQWGT 58
QY	124 IPSSSYDYVSFYLYQWAFIAAAAGTITSGSIAERTQFVAYLIYISPTTGFPYPVGVSHFWSP 183

```

; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10188
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10188

Query Match      18.3%; Score 483; DB 14; Length 446;
Best Local Similarity 28.7%; Pred. No. 1.3e-39;
Matches 129; Conservative 68; Mismatches 187; Indels 66; Gaps 10

QY 46 ADVNTYLLFSAYLVSQMGFAMLCAGSVRAKNTNMIMLTNVLDAAGLGFYFLFGFAPA 105
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 16 AANTGFMLICSALVIMTPGLAFFYGGVRVKSTLNLMWMSFISMGIVITLWLYGFSLA 75
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 106 FGSFNGFIG--KHFFGLKDI-----PSSSYD-YSYFELYQWAFATAAAAGITSGSIABRT 156
   ||| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 FGTOKGSLIGWTSDFVGTGIGKVEIWPVGVTIIPVYFATFQLMFAIITPAL:SGALADV 135
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 157 QFVAYLISFSLTGFVYVYVSHMFSPDGDWASAFKITDLRFTSGVIDFAGSGVVMVGGI 216
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 KFTAWSLFWALWATWYFVVAHVWVGTTGWA-----FDLGVIDFDAGGTAVHINAGA 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 217 AGLWALIEGPRMGFDFHAGRAVALRGHSASLVLCFTLLWFGWYGFNPGSFNKILLTYG 276
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 187 AALGVILVIGKRVG-----FKDPMRPHSLPLVNLGCGLLWFGWFGFNAGS----- 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 277 NSGNYQWMSAVGRTA-VTTTLAGSTAALTTLFGKRVISGHNVVTDVNCNLGGFPAITA 335
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 233 ---WLGNDGCGALMFINTQIATAAAMLAWLAYEKIRHGAFTTLGAASGAVAGLVAITP 288
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 336 GCSVVEPWAATVCGFVASIVLVIACNLKLABKVKDDPLEAAQLHGGCGTGWGVIPTALFAKK 395
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 289 SGAVSPDUGALVANGAIGVLCAMAVGLKYKFGYDDSLDVGVHLVCGVAGSLIIGFFASG 348
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 396 EYKVEVYGLGSAHLGLMG-----GGGKLLAAHVIIQILVTAGWVSWATMGPLFWG 443
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 349 G-----CQSDATGVFYGDHSFDQLWKCQAGVFAVLAYSILWSAILAFLIDKTIG----- 397
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 444 LNKLLKLRISSEDELAGWDMTRHGSGPAYAY 473
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 398 -----MRVSEDESIAGIDQAEHAETAYDF 421
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-09-801-368-192
; Sequence 192, Application US/09801368
; Patent No US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production i
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: US 09/487,558
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440

```

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SOFTWARE: Patent in version 3.0
SEQ ID NO 192
LENGTH: 492
TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
US-09-801-368-192

Query Match      17.0%; Score 449.5; DB 9; Length 492;
Best Local Similarity 27.9%; Pred. No. 3.4e-36;
Matches 121; Conservative 77; Mismatches 197; Indels 39; Gaps 10;

NY 51 YLLFSAYLVFMSQGLFAMLCAGSVRAKNTMIMLTNVLDAAGGLFYLYLGFAPF--GS 108
b 21 FMLGAALVFFVPGGLGYSLAERKSGALALIIVVLMATILVGLQWFMGYSLAFSKSA 80
Y 109 PMSGFICK-HFGQLKDIPSSYD-----YSYFLYQWAFALAAAGITSGSIAERTQFVAY 161
b 81 PNNKFCINLDSGFNNVYCKFDEDAYPELAYATFQMMFSCVNLIIAGATAERGLLPH 140
Y 162 LIYSSPLTGTVVYVSHWFSWPDGWSAPKTDRLFTSTGVIDPAGSGVVMVGGIAGMG 221
b 141 MVFLFLIATIGYCPVTYTIWSPGWA-----YQWGLDWAAGGNIETLSAVSGFVY 191
Y 222 ALLEGPRMGREFDHAGRAVALRGHSASLVLTGLFGLWFGWYFNPFSFKILLTYGNSGNY 281
b 192 SWFLGKRNKL-----LINFRHNVSLVLTGSLILWFGWLLFNAS-----SLSPNL 238
Y 282 YGOWSAVGRTAVTTLAGSTAALTTLFGKRVISGHNVTVCNGLLGGFAAITAGCSVVE 341
b 239 RSVY-APMNTCLSAITGGMTCWLLDYREK-----KWSTVGLCSGIISGLVAATPSSCIT 293
Y 342 PWAIVCGFVASIVLIACNKLAEKVKFDDPLEAAQLHGGCGTWGVIPTALFAKKEVYKEV 401
b 294 LYGLLQGVIVAGVVCNFATLKYAKYAKVDAMDILAEGHVGAVIGLIFNALFG-ADWIGM 352
Y 402 YGLGRAHGLMGGGKLLAAHVQILVITAGWVSATMGPFLFWGLNKL--KLIRISSEDELA 459
b 353 DGTTEHGGVWTHYKQYKQIAYIAASIGYTAATVITICFVGLVPGWRLRIRISEAEAA 412
Y 460 GMDWTRHGGGFAYAY 473
b 413 GMDQDQIGSFAYDY 426

RESULT 14
US-09-738-626-6981
; Sequence 6981, Application US/09738626
; Publication No. US20020137605A1
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, SATOSHI
; APPLICANT: MIZOGUCHI, HIROSHI
; APPLICANT: ANDO, SEIKO
; APPLICANT: HAYASHI, MIKIRO
; APPLICANT: OCHIAI, KEIKO
; APPLICANT: YOKOI, HARUHIKO
; APPLICANT: TATEISHI, NAKKO
; APPLICANT: SENOH, AKIHIRO
; APPLICANT: IKEDA, MASATO
; APPLICANT: OZAKI, AKIO
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-125
; CURRENT APPLICATION NUMBER: US/09/738,626
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: JP 99/377484
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: JP 00/159162
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 00/280988
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 7059
; SOFTWARE: Patent in ver. 3.0
; SEQ ID NO 6981
; LENGTH: 438
```

```
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-738-626-6981

Query Match      16.3%; Score 430.5; DB 9; Length 438;
Best Local Similarity 29.2%; Pred. No. 2.4e-34;
Matches 137; Conservative 68; Mismatches 177; Indels 87; Gaps 17;

QY 44 AFAYDNTYLLFSAYLVFMSQGLFAMLCAGSVRAKNTMIMLTNVLDAAGGLFYLYLGFPA 103
b 8 AVSGNSAWMLMSASLVLLMTPLALFYCGMSRQSKSVLNMWMSFGALGVVTVTYLLWGS 67
QY 104 PAFGSPS-----NGFTGKHFFGLKD-IPSSSYD-----SY-----FLYQWAFALAAAG 146
b 68 MSYGTQSIAGIFANPF--EFFGLKDSIVDADGNYIEGAAGYNIIDIGFOLTFAVISTA 124
QY 147 ITSISIAERTQFVAYLYSSPLTGTVVYVSHWFM-----SPDGWAS-AFKITDRLFS 198
b 125 LISGALAEVRFSTWLIFFSGAWTVLVYFPLAHMVWGGGLIGHNVTVGFASWLFSGTDEAN 184
QY 199 TGVTDPAAGSVVHMVGGIAGLWGLIEGPEMGREFDHAGRAVALRGHSASIVLGTFLWF 258
b 185 IAPIDFAGGTVVHLSAGTAALVLAIVGKR-----KTFGKAIA-RPHNLPWMLCAALLNF 239
QY 259 GWYGFNPQSFNKILLTYGNSGNYGOWSAVGRTAVTTLAGSTAALTTLFGKRVISGHN 318
b 240 GWFGFNGS-----AFAADG-----LAGLAWNTTAATAAAMLGWLATEKFRDGHAT 286
QY 319 VTDVNCNGLLGGFAITAGCSVVEPWAIVCGFVASIVLIACNKLAEKVK--FDDPLEAAQ 376
b 287 SIGAASGVVAGLVAVITPAAGALTPTVTSIIIGAIGGI--LACLGVLKRYRFGFDDSLDVVG 344
QY 377 LHGGCGTGMVFTTALFAKKEVYKEVYGLGRAHGLMGGGKLLAAHVQILV-----428
b 345 VHLVAGLWGTGVGGLATD-----IGWFSGGGMDGLKLFIVQIVIALVAVVFA 392
QY 429 -----IAGWVSATMGPFLFWGLNKLIRISSEDELAGMDWTRHGGGFAY 471
b 393 GVVITALLAFALKATVGT---W-----RVDDDVVEQQGIDTHEAESAY 430

RESULT 15
US-09-801-368-194
; Sequence 194, Application US/09801368
; Patent No. US20020128250A1
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. US20020128250A1man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.147
; CURRENT APPLICATION NUMBER: US/09/801,368
; CURRENT FILING DATE: 2001-03-07
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/160,587
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 194
; LENGTH: 499
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
```

US-09-801-368-194

```
Query Match      15.7%; Score 414; DB 9; Length 499;
Best Local Similarity 26.2%; Pred. No. 1.3e-32;
Matches 128; Conservative 73; Mismatches 207; Indels 80; Gaps 17;

Qy 59 VFSMQLGFAMLCAGSVRAKNTNMIMLTNVLDAAGGLFYLLFGFAPAF--GSPSNGFIGK 116
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 42 VMIWVPGIGLLYGLSRKHALSLLWASMASAVCIQWFFWGYSLAFSHNTRNGNFIGT 101
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 117 -HFGGLKDI-----PSSSYDYFYFLYONAPATAAAGITSGIAERTQFVAYLIYSSPLT 169
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 102 LEFFGFNFVLGAPSSVSSLPDILFAYVYQGFMAAVTGALMLGGACERARLPFMMVFLFLMM 161
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 170 GFVYPVWVSHWFSPDGWASAFKITDRLFSTGVIDFAGSGVWVMVGGIAGLWGALIEGPRM 229
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 162 TIVYCPPIACWVNAEGW-----LVKLGSLDYAGGLCVHLTSGHGLVYVALLIGKRN 212
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 230 GRFDHAGRAVALRGHSASLVVLGTFLLWFGWYGFNPGSFNKILLITYGNSGN-YYQWSAV 288
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 213 DPVTRKGP-KYKPHSVTSVVLGTVFLWFGWMPFNGS-----AGNATIRAWYSI 261
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 289 GRTAVTTTLAGSTAALTFL-----GKRVISGHMNVTVDCNGLLGGFAAITAGCSVVEP 342
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 262 ----MSTNLAAACGGLTWVIDYFCGRK-----WTVGLCSGIAGLVGITPAAGFVPI 312
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 343 WAAIVCGFVASIVLIACN---KLAEKVKFDDPLEAAQLHGGCGTGWGVIETALFAKKEYVK 399
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 313 WSAVVIQVWTG---AGCNLAVDLKSLLRIDDLDCYSIHVGVCIGSVLTGIFA-ADYVN 368
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 400 EYVG--LGRAHGLLMGGGKLLAAHVIOILVIAGVYSATWGPFLFWGLNKLK--LRISSE 455
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 369 ATAGSYISPIDGGWINHHYKQVGYQLAGICAALAWTVVTSILLTMNAIPFLKLELSAD 428
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 456 DELAGMDMTRHGGPAY---AY-----EDETCHKHGMQLRRVGN 491
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 429 EEELGTDAQAQIGFTYBESTAYIPEIRSKTSAQMPPPHENIDDKIVGNTDAEKNSTPSD 488
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 492 ASSTPTTD 499
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 489 ASSTKNTD 496
   ||| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
```

Search completed: March 9, 2004, 12:01:17
Job time : 41 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

XM protein - protein search, using sw model

Run on: March 9, 2004, 11:52:48 ; Search time 17 Seconds
(without alignments)
1531.475 Million cell updates/sec

Title: US-10-033-109-4

Perfect score: 2639

Sequence: 1 MSLLPACPAEQALQLGPNTT.....HGMQLRVGNASPTTDE 500

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2129.5	80.7	501	AT11_ARATH	P54144 arabidopsis
2	2089.5	79.2	488	AT11_LYCES	P58905 lycopersico
3	2011	76.2	519	AT13_ARATH	Q98q9 arabidopsis
4	1973.5	74.8	504	AT14_ARATH	Q9svt8 arabidopsis
5	1953	74.0	514	AT12_LYCES	O04161 lycopersico
6	1919	72.7	514	AT12_ARATH	Q9zpj8 arabidopsis
7	1591	60.3	450	AT13_LYCES	Q9fm0 lycopersico
8	706	26.8	534	AMT1_CAEEL	P54145 caenorhabdi
9	703	26.6	507	Y108_SYNY3	P54147 synchocyst
10	678.5	25.7	442	YAI7_SYNY3	P72935 synchocyst
11	579.5	22.0	687	AMT3_CAEEL	Q21565 caenorhabdi
12	569.5	21.6	541	Y537_SYNY3	P54148 synchocyst
13	496	18.8	477	AMT_MYCTU	Q10968 mycobacteri
14	494	18.7	404	NRG3_BACSU	Q07429 bacillus su
15	485	18.4	420	YD43_METJA	Q58739 methanococc
16	470	17.8	428	AMTB_ECOLI	P37905 escherichia
17	460	17.4	407	Y661_METTH	Q26757 methanobact
18	457	17.3	423	AMT_AQUAE	Q66515 aquifex aeo
19	456.5	17.3	412	Y663_METTH	Q26759 methanobact
20	454.5	17.2	554	MEP1_CAEEL	Q20605 caenorhabdi
21	449.5	17.0	492	AMT2_YEAST	P40260 saccharomyc
22	446	16.9	489	MEP3_YEAST	P53390 saccharomyc
23	436	16.5	391	Y058_METJA	Q60366 methanococc
24	414	15.7	499	MEP2_YEAST	P41348 saccharomyc
25	366	13.9	475	AMT2_ARATH	Q9m6n7 arabidopsis
26	363.5	13.8	452	AMT_CORGL	P54146 corynebacte
27	127.5	4.8	455	Y003_BACSU	P42237 bacillus su
28	126	4.8	409	RHAG_HUMAN	Q02094 homo sapien
29	124.5	4.7	353	RHL_HVLP1	Q28446 hylobates p
30	124	4.7	416	RHL_WACMU	Q28849 macaca mla
31	123.5	4.6	444	GARP_ECOLI	P42613 escherichia
32	121.5	4.6	456	Y003_BACSU	P42205 pseudomonas
33	119	4.5	534	TNA1_YEAST	P53322 saccharomyc

RESULT 1

ID	AT11_ARATH	STANDARD;	PRT;	501 AA.
AC	P54144;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Ammonium transporter 1, member 1 (AtAMT1;1).			
GN	AMT1.1 OR AT4G13510 OR T6G15.60.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID:3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Landsberg erecta;			
RX	MEDLINE-94341958; PubMed-8062823;			
RA	Ninnemann O., Janniaux J.-C., Frommer W.B.;			
RT	"Identification of a high affinity NH4+ transporter from plants.";			
RL	EMBO J. 13:3464-3471(1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=cv. Columbia;			
RX	MEDLINE-20083488; PubMed-10617198;			
RA	Mayer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,			
RA	Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terryn N.,			
RA	Harris B., Ansong W., Brandt P., Grivell L.A., Rieger M.,			
RA	Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,			
RA	Kreis M., Dalseny M., Puigdomenech P., Watson M., Schmidtheini T.,			
RA	Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,			
RA	Vos P., Hoheisel J., Zimmermann W., Wedler H., Ridley P.,			
RA	Langham S.-A., McCullagh B., Bilham L., Robben J.,			
RA	Van der Schueren J., Grymonprez B., Chuang Y.-J., Vandenbussche P.,			
RA	Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoor E.,			
RA	Weitzenegger T., Bothe G., Ramepberger U., Hilbert H., Braun M.,			
RA	Holzer E., Brandt A., Peters S., van Staveren M., Dirkse W.,			
RA	Moelmaier P., Klein Lankhorst R., Rose M., Hauf J., Koetter P.,			
RA	Berneiser S., Hempel S., Feldpausch M., Lamberth S., Van den Daele H.,			
RA	De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,			
RA	Van Montagu M., Rogers J., Cronin A., Quail M.A., Bray-Allen S.,			
RA	Clark L., Doggett J., Hall S., Kay M., Lennard N., McLay K., Mayes R.,			
RA	Pettett A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,			
RA	Borkova D., Bloedeker H., Scharfe M., Grimm M., Loehnert T.-H.,			
RA	Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,			
RA	Gabel C., Fuchs M., Fartmann B., Graendath K., Dauner D., Herzl A.,			
RA	Neumann S., Argiriou A., Vitale D., Liguori R., Piravandi E.,			
RA	Massenet O., Quigley F., Clabaud G., Leuchner A., Aebischer S.,			
RA	Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,			
RA	Cheford F., Cooke R., Berger C., Monfort A., Casacuberta E.,			
RA	Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,			
RA	Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,			
RA	Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Biele C.,			
RA	Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,			
RA	Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,			
RA	Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Spiegel L.,			

P18696 emericella
Q28427 gorilla gor
P77610 escherichia
Q28481 macaca fasc
Q28426 gorilla gor
P40812 esalmonella
P09836 escherichia
P72060 mycobacteri
Q02161 homo sapien
P37514 bacillus su
Q47689 escherichia
O52733 lactobacill

ALIGNMENTS

119	DB	PTASADYSNELYQWAFIAAAGITSGSIAERTQFVAYLIYSSELTGFVYPVWSFWFSVD	178
185	QY	GWASAFKIT-DRLFSTGVTDIFAGSGVYHVMVGIAIGKALIEGPRMGSEFDHAGRAVALRG	243
179	DB	GWASPFPTDGLLFSTGAIDFAGSGVYHVMVGIAIGKALIEGPRMGSEFDHAGRAVALRG	238
244	QY	HSASLVVLGTFLLWFGWYGFNPGSFNKKILLTYGNSGNTYQWGSVAVGRTAVTTTLAGSTAA	303
239	DB	HSASLVVLGTFLLWFGWYGFNPGSFNKKILVTV-ETGTYNGQWSAVGRTAVTTTLAGCTAA	297
304	QY	LTTLFGKRVISGHWNVTDCVGLLGSGFAITAGCSVWEPWAAI VCGFVASIVLIACNKL A	363
298	DB	LTTLFGKRLSGHWNVTDCVGLLGSGFAITAGCSVWEPWAAI ICGFVAALVILGCKNLA	357
364	QY	EKVFDDPLEAALHGCGGTGVIPTALFAKXEYKVEYVG--LGSAGLLMGGGGKLLAA	421
358	DB	EKLKYDDPLEAALHGCGCGAWGLIFTALFAQSKYLNQIYGNKPGSPHGLFVGGGGKLLGA	417
422	QY	HVIOILVIAGVSNATGCPFWGLINKLKLRISSSEDELAGMDMTRHGGFAYAY-EDDETHK	480
418	DB	QLIQIIVITGVSNATGTTFFILKOKKLRISSSEDELAGMDMTRHGGFAYMYFDDDESHK	477
481	QY	HGMQLRRVGP-----NASSTPT 497	
478	DB	AIQLRRVPEPSPPSGANTTPT 499	
RESULT 2			
ATIL_LYCES			
AD	ATIL_LYCES	STANDARD; PRT; 488 AA.	
IC	P58905;		
DT	28-FEB-2003	(Rel. 41, Created)	
DT	28-FEB-2003	(Rel. 41, Last sequence update)	
DT	10-OCT-2003	(Rel. 42, Last annotation update)	
DE	Ammonium transporter 1, member 1 (LeAMT1;1).		
GN	NCBI_TaxID=4081;		
OS	SEQUENCE FROM N.A.		
OS	LYCopersicon esculentum (Tomato).		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;		
OC	Lamiales; Solanales; Solanaceae; Solanum.		
ON	NCBI_TaxID=4081;		
OX	[1]		
RP	MEDLINE=96353959; PubMed=8755617;		
RP	Lauter F.-R., Ninnemann O., Bucher M., Riesmeier J.W., Frommer W.B.;		
RA	"preferential expression of an ammonium transporter and of two		
RT	putative nitrate transporters in root hairs of tomato.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 93:8139-8144 (1996).		
RL	[2]		
RP	INDUCTION.		
RP	MEDLINE=20208060; PubMed=10743657;		
RP	von Witen N., Lauter F.-R., Ninnemann O., Gillissen B., Walch-Liu P.,		
RA	Engels C., Jost W., Frommer W.B.;		
RT	"Differential regulation of three functional ammonium transporter		
RL	genes by nitrogen in root hairs and by light in leaves of tomato.";		
RL	Plant J. 21:167-175 (2000).		
CC	-!- FUNCTION: Involved in high affinity ammonium uptake.		
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).		
CC	-!- TISSUE SPECIFICITY: Root hairs and leaves.		
CC	-!- INDUCTION: By nitrogen deficiency.		
CC	-!- SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49)		
CC	family.		
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CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (see http://www.isb-sib.ch/announcement		
CC	or send an email to license@isb-sib.ch).		
CC	EMBL; X52854; -; NOT_ANNOTATED_CDS.		
CC	OR		


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301 TAALTTLFGKRRVISHWNTVDVNCGLLGGFAAITAGCSVVEPWAIVCGFVASIVLIACN 360
306 TAALTTLFGKRLDGYWNTVDVNCGLLGGFAAITSGCSVVEPWAIVCGFVAAWLMGCN 365
361 KLAEKVKFDDPLEAAOLHGGCGTWGVIPTALFAKKEVYKEVYG--LGRAHGLMGGGSKL 418
366 RLAEKQKQFDDPLEAAOLHGGCGGAWGIIPTGLFAEKRYIAEIEGGDPNPFGLLMGGGGRLL 425
419 LAARHVIQILVIAGWSATMGPFVFWGLNKLKLRISSSEDELAGMDTRGGFAYAYEDED 478
426 LAARHVIQILVIAGWSVMTGTLFFILHLKLRLPAEDIEAGVDTSHGGLAYMYTDEI 485
479 HKHGMQLRRVG-----PN 491
486 -RNGIMVRRVGGNDNPN 501

RESULT 5
AT12_LYCES
ID AT12_LYCES STANDARD; PRT; 514 AA.
AC 004161;
JT 15-JUL-1998 (Rel. 36, Created)
JT 15-JUL-1998 (Rel. 36, Last sequence update)
JT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ammonium transporter 1, member 2 (LeAMT1;2).
EN AMT1.2
DS Lycopersicon esculentum (Tomato).
DC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
DC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
DC Lamnids; Solanales; Solanaceae; Solanum.
DX NCBI TaxID=4081;
UN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Root hairs;
RX MEDLINE=20208060; PubMed=10743657;
XA von Wiren N., Lauter F.-R., Ninnemann O., Gillissen B., Walch-Liu P.,
RA Engels C., Jost W., Frommer W.B.;
RT "Differential regulation of three functional ammonium transporter
genes by nitrogen in root hairs and by light in leaves of tomato.";
RL Plant J. 21:167-175(2000).
CC - FUNCTION: Involved in high affinity ammonium uptake.
CC - SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC - TISSUE SPECIFICITY: Root hairs and leaves.
CC - INDUCTION: By nitrogen. Highest expression after onset of
light.
CC - SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49)
family.
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or send an email to license@isb-sib.ch).
CC EMBL; X95098; CAA64475.1; -.
DR PIR; T06585; T06585.
DR InterPro; IPR001905; Ammonium transp.
DR Pfam; PF00909; Ammonium transp; 1.
DR TIGRfams; TIGR00836; ant; 1.
DR PROSITE; PS01219; AMMONIUM_TRANSP; 1.
KW Transport; Transmembrane; Multigene family.
FT TRANSMEM 52 72 POTENTIAL.
FT TRANSMEM 87 107 POTENTIAL.
FT TRANSMEM 133 153 POTENTIAL.
FT TRANSMEM 158 178 POTENTIAL.
FT TRANSMEM 205 225 POTENTIAL.
FT TRANSMEM 249 269 POTENTIAL.
FT TRANSMEM 290 312 POTENTIAL.
FT TRANSMEM 316 336 POTENTIAL.
FT TRANSMEM 342 362 POTENTIAL.
FT TRANSMEM 375 395 POTENTIAL.

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FT TRANSMEM 428 448 POTENTIAL.
SQ SEQUENCE 514 AA; 55543 MW; 9987FE9FE17173C9 CRC64;
Query Match 74.0%; Score 1953; DB 1; Length 514;
Best Local Similarity 75.3%; Pred. No. 3.3e-129;
Matches 379; Conservative 43; Mismatches 71; Indels 10; Gaps 7;
QY 2 SLPACPAEOLAQLGNTDTASAAASLICGHFAAVDSKFVDTAFADVNTYLLPSAYLVFS 61
DB 3 SAMTCSAAELFPHLG--SSANATAAAEFICSRFSAYSEYLTNTTYAVDTTLLYLSAYLVFA 61
QY 62 MOLGGFAMLCAGSVRAKNTNIMLTNVLDAAGGLFYLLFGFAFAGFSPSNGFICKHFFGL 121
DB 62 MOLGGFAMLCAGSVRAKNTNIMLTNVLDAAGGSSYLLFGFAFAGFSPSNGFICKHFFGL 121
QY 122 KOIPSSSYDYFLYQWAFATAAGITSGSAERTQFVAYLIYSSFLTGFVYVYVSHFW 181
DB 122 KEFPFQAFDYSYFLYQWAFATAAGITSGSAERTQFVAYLIYSSFLTGFVYVYVSHFW 181
QY 182 SPDGWASAFKIID--RLPSTGVIDFAGSVVHMVGGIAGLWGLIEGPRMGRFDPHAGRAV 239
DB 182 SGGGWASASK-TDGNLLRLRFVVIDFAGSVVHMVGGIAGLWGLIEGPRMGRFDRSGSV 240
QY 240 ALRGHSASLVLGTFTLLFMFGMYGFPNGFNKILTYGNS--GNYYGQMSAVGRTAVTTTL 297
DB 241 ALRGHSASLVLGTFTLLFMFGMYGFPNGFNKILTYGNS--GNYYGQMSAVGRTAVTTTL 300
QY 298 AGSTAALTTFLGKRVISGHMNVTVDCNGLLGGPAITAGCSVVEPWAIVCGFVASIVLI 357
DB 301 AGCTAALTTFLCKRLVLAHNVVDVDCNGLLGGPAITAGCSVVEPWAIVCGFVASIVLI 360
QY 358 ACNKLAEKVKFDDPLEAAQLHGGCGTGWVIFTALFAKKEVYKEVY--GL-GRAHGLLMGGG 415
DB 361 GFNALAAKLKYYDDPLEAAQLHGGCGSGWIIPTGLFAKKEVYKEVYVPGFNPYPGLFMGGG 420
QY 416 GKLLAAHVLIQILVIAGWSATMGPFVFWGLNKLKLRISSSEDELAGMDTRGGFAYAY-- 473
DB 421 GKLLGQVIVQVVIIGWVSVTNGPLFYLLHLKFLRLSRDDETAGMDLTRHGGFAYIYHD 480
QY 474 EDDETHKHGMQLRRVGPNASSTP 496
DB 481 EDEGSSMPGFKMTRVEPTNTSTP 503

RESULT 6
AT12_ARATH
ID AT12_ARATH STANDARD; PRT; 514 AA.
AC Q9ZPJ8; Q9SOH8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ammonium transporter 1, member 2 (AtAMT1;2).
GN AMT1.2 OR ATIG64780 OR F13011.9.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OC NCBI_TaxID=3702;
UN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=cv. C24; TISSUE=Seed;
RX MEDLINE=99264313; PubMed=10330477;
RA Gazzarrini S., Lejay L., Gojon A., Ninnemann O., Frommer W.B.,
RA von Wiren N.;
RA "Three functional transporters for constitutive, diurnally regulated,
and starvation-induced uptake of ammonium into Arabidopsis roots.";
RL Plant Cell 11:937-948(1999).
UN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. C24; TISSUE=Root;
RA Shelden M.C., Howitt S.M., Udvardi M.K.;
RA "Arabidopsis thaliana AtAMT1;2 from N-deprived roots.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.

```

[3]
 SEQUENCE FROM N.A.
 STRAIN=cv, Columbia;
 MEDLINE=21016719; PubMed=11130712;
 2A Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 2A White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
 2A Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 2A Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 2A Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 2A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
 2A Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 2A Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
 2A Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 2A Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
 2A Miitscher J., Miranda M., Nguyen J., Nierman W.C., Osborne B.I.,
 2A Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 2A Sakano H., Saltzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 2A Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 2A Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
 2A Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 2A "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 2A thaliana";
 2A Nature 408:816-820 (2000).
 [4]
 SEQUENCE FROM N.A.
 STRAIN=cv, Columbia;
 MEDLINE=22954850; PubMed=14593172;
 2A Yamada K., Lim J., Dale J.M., Chen H., Shinn P., Palm C.J.,
 2A Southwick A.M., Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,
 2A Karlin-Newman G., Liu S.X., Lam B., Sakano H., Wu T., Yu G.,
 2A Miranda M., Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,
 2A Chan M.M., Tang C.C., Onodera C.S., Deng J.M., Akiyama K., Ansari Y.,
 2A Arakawa T., Banh J., Banno F., Bowler L., Brooks S.Y., Carninci P.,
 2A Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,
 2A Hayashizaki Y., Johnson-Hopson C., Heuan V.W., Iida K., Karnes M.,
 2A Khan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,
 2A Kamiya A., Meyers C., Nakajima M., Narusaka M., Seki M., Sakurai T.,
 2A Satou M., Tamers R., Vaysberg M., Wallender E.K., Wong C., Yamamura Y.,
 2A Yuan S., Shinohara K., Davis R.W., Theologis A., Ecker J.R.;
 2A "Empirical analysis of transcriptional activity in the Arabidopsis
 2A genome";
 2A Science 302:842-846 (2003).
 CC -!- FUNCTION: Involved in high affinity ammonium uptake.
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- TISSUE SPECIFICITY: High expression in root.
 CC -!- SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49)
 CC family.

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 DR EMBL: AF083036; AAD54639.1; -
 DR EMBL: AF110721; AAD17001.1; -
 DR EMBL: AC006193; AAD38253.1; -
 DR EMBL: AY062571; AAL32649.1; -
 DR EMBL: AY093374; AAM13373.1; -
 DR PIR: A96671; A96671.
 DR InterPro: IPR001905; Ammonium transp.
 DR Pfam: PF00909; Ammonium transp; 1.
 DR PROSITE: PS01219; AMMONIUM_TRANSP; 1.
 DR TRANSMEM 56 76
 TRANSMEM 91 111
 TRANSMEM 140 160
 TRANSMEM 165 185
 TRANSMEM 212 232
 TRANSMEM 257 277
 TRANSMEM 257 277

FT TRANSMEM 291 313 POTENTIAL.
 FT TRANSMEM 328 348 POTENTIAL.
 FT TRANSMEM 351 371 POTENTIAL.
 FT TRANSMEM 380 400 POTENTIAL.
 FT TRANSMEM 431 451 POTENTIAL.
 FT DOMAIN 18 26 POLY-SER.
 FT CONFLICT 198 198 R -> G (IN REF. 1).
 FT CONFLICT 310 310 A -> S (IN REF. 1).
 FT CONFLICT 438 438 V -> I (IN REF. 1).
 SQ SEQUENCE 514 AA; 55013 MW; 86C3C61F044A0CC6 CRC64;
 Query Match 72.7%; Score 1919; DB 1; Length 514;
 Best Local Similarity 73.7%; Pred. No. 7.9e-127;
 Matches 370; Conservative 48; Mismatches 74; Indels 10; Gaps 6;
 QY 6 CBAEQIAQL--GPNTTASAAALICGHEAARVSKFVDTAFADNTYLLFSAVLVFSMQ 63
 DB 8 CBAVDLSALLSSSSNSTSLAATFLCSQINISNKLSDTYAIVDNTYLLFSAVLVFSMQ 67
 QY 64 LGFAMLCAGSVEAKNTMIMLTNVLDAAGGLFYLLFGFAPAFGSPNGFTGKH--PFGL 121
 DB 68 LGFAMLCAGSVEAKNTMIMLTNVLDAAGGLFYLLFGFAPAFGSPNGFTGKH--PFGL 127
 QY 122 KDIIPS--SSYDYSFELYQWAFATAAGITSGSIARTOPVAVLIYSSFLTGPVYVPSHWF 180
 DB 128 SSYPERPDSFDFLYQWAFATAAGITSGSIARTOPVAVLIYSSFLTGPVYVPSHWF 187
 QY 181 WSPDQWASAFKITDR-LFSTGVDFPAGSVVHVMYGGIAGLWGLIEGRMRGPFHAGRAV 239
 DB 188 WSDGDWASASRDNLLFGSGAIDFAGSVVHVMYGGIAGLWGLIEGRMRGPFHAGRAV 247
 QY 240 ALRGHSASLVILGTLLWFGWGFNPGSNKILLTYGNSGNYGQWAVGRTAVTTTLG 299
 DB 248 ALRGHSASLVILGTLLWFGWGFNPGSNKILLTYGNSGNYGQWAVGRTAVTTTLG 307
 QY 300 STAAATLTFGKEVISCHWNVTIDVNCNLLGSGFAAITAGCSVVEPWAAIVCGFVASIVLIAC 359
 DB 308 CTAATLTFSGKLLAGHNVNIDVNCNLLGSGFAAITAGCSVVEPWAAIVCGFVASIVLIAC 367
 QY 360 NKLAEKVKDDPLEAAQLHGGCGTGWVFTALPAKKEVYKVEYGLGRAHGLMGSGKLL 419
 DB 368 NLLAKKLYDDPLEAAQLHGGCGANGLIPTGLFARKEYVNIYSGDRPYGLFMGGKLL 427
 QY 420 AAHVIOILVIAGWVSATMGPLFWGLNKLKLLRISSDELAGMDTRGGGFAYAYEDDE-- 477
 DB 428 AAQIVQIIVVGWVTVTGWPLFYGLHKNNLRLISAEDEMAGMDTRGGGFAYAYEDDV 487
 QY 478 -THKGQQLRRVGPNA-SSTPT 497
 DB 488 STKPMGHFAGRYEPTSRSTPT 509
 RESULT 7
 AT13_LYCES STANDARD; PRT; 460 AA.
 AC Q9FVNO;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ammonium transporter 1, member 3 (LeaMT1.3).
 GN AMT1.3.
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamiales; Solanales; Solanaceae; Solanum.
 CX NCBI_TaxID=4081;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Leaf;
 RX MEDLINE=20208060; PubMed=10743657;
 RA von Wieren N., Lauter P.-R., Ninnemann O., Gallissen B., Walch-Liu P.,
 RA Engels C., Jost W., Frommer W.B.;
 RA "Differential regulation of three functional ammonium transporter

RT genes by nitrogen in root hairs and by light in leaves of tomato.";
RL Plant J. 21:167-175(2000).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Leaves.
CC -!- INDUCTION: Highest expression in darkness.
CC -!- SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49) family.

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CC EMBL; AF118858; AAG11397.1; .
DR InterPro; IPR001905; Ammonium transp.
DR Pfam; PF00909; Ammonium transp; 1.
DR TIGRfams; TIGR00836; amt; 1.
DR PROSITE; PS01219; AMMONIUM_TRANS; 1.
KW Transport; Transmembrane; Multigene family.
FT TRANSMEM 15 37 POTENTIAL.
FT TRANSMEM 50 72 POTENTIAL.
FT TRANSMEM 98 117 POTENTIAL.
FT TRANSMEM 124 146 POTENTIAL.
FT TRANSMEM 166 188 POTENTIAL.
FT TRANSMEM 209 227 POTENTIAL.
FT TRANSMEM 255 277 POTENTIAL.
FT TRANSMEM 305 327 POTENTIAL.
FT TRANSMEM 337 356 POTENTIAL.
FT TRANSMEM 377 399 POTENTIAL.
SQ SEQUENCE 460 AA; 49652 MW; 6D9CF6C2C2395BA CRC64;

Query Match 60.3%; Score 1591; DB 1; Length 460;
Best Local Similarity 67.2%; Pred. No. 5.5e-104;
Matches 301; Conservative 56; Mismatches 81; Indels 10; Gaps 5;

2Y 46 AVDNTYLLFSAYLVFMSQGLFAMLCAGSVRAKNTMIMLTNVLDAAGGLFYLRGFAPA 105
D 12 SINAIYLLFSAYLVFVQGLFAMLCAGSVRAKNTMIMLTNVLDAAGGLFYLRGFAPA 71
2Y 106 PGSPNGFIKHFGLKDIIPSSYDYSLYQWAFAPAAAGITSGSIABRTQFVAYLYS 165
D 72 FGD-SNPFICASYFALKDIPSSYDYSLYQWAFAPAAAGITSGSIABRTQFVAYLYS 130
Y 166 SFLTGFVYVYVSHWFSPDGNWASAFKIDTDLFTGTVIDFAGSVVHMVGGLAGLWGLALIE 225
D 131 FFLTGFVYVYVSHWFSPDGNWASAFKIDTDLFTGTVIDFAGSVVHMVGGLAGLWGLALIE 189
Y 226 GPRVGRFDHAGRAVALRGHSASLVLTGTLFWTGWYGFNPGSNKILLTYGNSGNYGQW 285
D 190 GPRVGRFDHAGRAVALRGHSASLVLTGTLFWTGWYGFNPGSNKILLTYGNSGNYGQW 248
Y 286 SAVGRTAVTTTLTLAGSTAALTLFGKRVISGHVNVTDVNCGLLGGFAAITAGCSVVEPMAA 345
D 249 TSVGRTAVTTTLTLAGSTAALTLFGKRVISGHVNVTDVNCGLLGGFAAITAGCSVVEPMAA 308
Y 346 IVCGFVASIVLIACNKLAEKVKDDPLEAAQLHGGCGTGWVIFTALPAKKEYKVEYIGLG 405
D 309 ILCGFCAAVILGLENILAKFKEDDPLEAAQLHGGCGTGWVIFTALPAKKEYKVEYIGLG 368
Y 406 -----RAHGLLGGGKLLAAHVLIQILVIAGVVSATMGLFWGLNKLKILIRISSEDEL 460
D 369 KTIIRPSGLLGGGGLGFLGAQIVELLUSIVVWSLTNGPLFYLLQKLILIRISSEDEL 428
Y 461 DMTRHGGGFAY--AYEDDETHKHGMQLR 486
D 429 LDISSHGGYAYDASQESNARFFGEYLR 456

RESULT 8
AMT1_CAEEL

ID AMT1_CAEEL STANDARD; PRT; 534 AA.
AC P54145;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative ammonium transporter C05E11.4.
GN C05E11.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoides;
OC Rhabditidae; Peloderinae; Caenorhabditis.
CX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Geisel C.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Involved in the uptake of ammonia (Probable).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -!- SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49) family.

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CC EMBL; U53338; AAA96191.1; .
DR PIR; T15414; T15414.
DR WormPep; C05E11.4; CE06770.
DR InterPro; IPR001905; Ammonium transp.
DR InterPro; IPR008960; CBD9-like.
DR Pfam; PF00909; Ammonium transp; 1.
DR TIGRfams; TIGR00836; amt; 1.
DR PROSITE; PS01219; AMMONIUM_TRANS; 1.
KW Hypothetical protein; Transport; Transmembrane.
FT TRANSMEM 31 51 POTENTIAL.
FT TRANSMEM 69 89 POTENTIAL.
FT TRANSMEM 115 135 POTENTIAL.
FT TRANSMEM 139 159 POTENTIAL.
FT TRANSMEM 184 204 POTENTIAL.
FT TRANSMEM 223 243 POTENTIAL.
FT TRANSMEM 263 283 POTENTIAL.
FT TRANSMEM 291 311 POTENTIAL.
FT TRANSMEM 318 338 POTENTIAL.
FT TRANSMEM 346 366 POTENTIAL.
FT TRANSMEM 401 421 POTENTIAL.
SQ SEQUENCE 534 AA; 58490 MW; C17CFE44E0DC3D05 CRC64;

Query Match 26.8%; Score 706; DB 1; Length 534;
Best Local Similarity 36.0%; Pred. No. 3.7e-42;
Matches 164; Conservative 74; Mismatches 185; Indels 32; Gaps 9;

QY 41 VDTAF--AVDNTYLLFSAYLVFMSQGLFAMLCAGSVRAKNTMIMLTNVLDAAGGLFY 98
D 21 LETGFVENVNSPFLCSMALIIFMQCGFAYLEAGVRSKNTNLIKRLDSCICIIQW 80
Y 99 LFGFAFAPGSPNG---FTGKHFGLKDIIPSSYDYSLYQWAFAPAAAGITSGSIABRT 155
D 81 AIGMALAYGDSGSGVNLFGVHSQFFL---SGFSYDPRFFQYVFSATAATVSGAVER 136
Y 156 TQFVAVLYSSFLTGTVPVSHWSPDGNWASAFKIDTDLFTGTVIDFAGSVVHMVG 215
D 137 CEFITVYCTVISTFIYVPLTHWGTENGW-MAGKITSIGIIDTKYDDFAGSGLVLCGG 195
Y 216 IAGLWGLALIEGPRMGRF--DHAGRAVALRGHSASLVLTGTLFWGLNKLKILIRISSE 273
D 196 SISFLAAMINGPRIGKFPDDEDEDEILGHVSPFTALGGFLMGFLAFNGGVSASI-- 253
Y 274 TYGNSGNYGQWASVORTAVTTTLAGSTAALTLFGKRVISGHVNVTDVNCGLLGGFAAI 333

254 -----SHAGDGHVALAMINTILSFAFAALIYLVGHVYQHGKWTLLLTINACLSGMVAA 307
 334 TAGCSVVEWAAIVCGFVASIVLIACNKLAERKVEDDPLEAAQLHGGGCTMGVFTALFA 393
 308 CAGCNKEWACITWGLGAGLIYLAFLSKLMIELKIDDDPLDAFVHAGGGFWGLMSSSIIS 367
 394 KKEYVEVTVGLGRAHGLLMGGGKLLAA-----HVIQILVIAGVNSATMGPLFWGLNKL 447
 368 ---HGGVAYALADAVSAGKNSGDHLTOFAQLGWQMICALAIIMSGLWMLPIFWILKKT 424
 448 KLLRISSEDELAGMDWRHGGFAYAYEDDETHKHG 482
 425 GKLRSVEEVEINGLDVFKHGEWAYPL--RAYCHG 456

RESULT 9

(108 SYN3
 ID Y108 SYN3 STANDARD; PRT; 507 AA.
 AC PS4147;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Putative ammonium transporter sll0108.
 SN SLL0108.
 SS Synchocystis sp. (strain PCC 6803).
 SC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
 SX NCBI_TaxID=1148;
 SN SLL0108.
 RP SEQUENCE FROM N.A.
 MEDLINE=96127529; PubMed=8590279;
 RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
 RA Sugita M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synchocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
 RT region from map positions 64% to 94% of the genome.";
 RL DNA Res. 2:153-166(1995).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49)
 CC family.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D64004; BAA10631.1; --
 CC PIR; S76687; S76687.
 CC InterPro; IPR001905; Ammonium transp.
 CC Pfam; PF00909; Ammonium transp; 1.
 CC TIGRFAMs; TIGR00836; ant; 1.
 CC PROSITE; PS01219; AMMONIUM_TRANSP; 1.
 KW Hypothetical protein; Transport; Transmembrane; Complete proteome.
 FT TRANSMEM 44 64 POTENTIAL.
 FT TRANSMEM 90 110 POTENTIAL.
 FT TRANSMEM 128 148 POTENTIAL.
 FT TRANSMEM 154 174 POTENTIAL.
 FT TRANSMEM 178 198 POTENTIAL.
 FT TRANSMEM 211 231 POTENTIAL.
 FT TRANSMEM 245 265 POTENTIAL.
 FT TRANSMEM 286 306 POTENTIAL.
 FT TRANSMEM 315 335 POTENTIAL.
 FT TRANSMEM 347 367 POTENTIAL.
 FT TRANSMEM 370 390 POTENTIAL.
 FT TRANSMEM 399 419 POTENTIAL.
 FT TRANSMEM 438 458 POTENTIAL.
 SEQUENCE 507 AA; 53580 MW; 1840AE99FFA08E6A CRC64;

Query Match 26.6%; Score 703; DB 1; Length 507;
 Best Local Similarity 36.2%; Pred. No. 5.7e-42;
 Matches 160; Conservative 63; Mismatches 173; Indels 46; Gaps 8;

QY 51 YILFSAYLVFQSMQLGFAMLCAGSVRAKNTWNIMLTNVLDAAGGLFYFLFGFAFAFGSPS 110
 DB 92 WLIILAAIIVFEMNAGFGMLTGLCRQKNVNIILTKNLIVPALATIAYWAGFSLMFGSSG 151
 QY 111 NGFI-----GKHF-FGLKDIPISSSDYSLYQWAFIAAAGITSGSIAERTOFVAY 161
 DB 152 NFVFGCGFFLSGHTNYGLSPFPEGLPVAVFELPVAFSATAATIVSGAVAEIRKNEF 211
 QY 162 LIYSFSLFGFYVYVSHWFSPDGWASAFKITDRLPSTGTVIDFAGSGVVMVGGIAGLWG 221
 DB 212 LIFSLLVGLIAYPITGHVWWDAGW-----LYTMGFMDFAGSTVWHSVGGWALAG 262
 QY 222 ALIEGPRMGREDHAGRAVALRGHSASLVLTGTLTFWEGYGFNPSPENKILLTYGNSGY 281
 DB 263 AFLGLPRLGKFDV-GRPGAIPGNHNGFAMLCGLILNIGWFGFNFGS-----Q 308
 QY 282 YQWSAVGRTAVTTTLAGSTAALTTLFGKRVISGHMNVTVDCNGLLGGPFAAITAGSVVE 341
 DB 309 LAADOACAVIATVNTLAASAGGLTATFTSLKDGKPLDTWVINGVLAGLVITAGCAGVS 368
 QY 342 PWAIVCGFVASIVLIACNKLAERKVEDDPLEAAQLHGGGCTMGVFTALFAKVEYKEV 401
 DB 369 YWGSVIIGIAGILVYVSVAFDKIKDDPVGALSVHLVNGVWGTLAGVFNMEK----- 423
 QY 402 YGLGRAHGLMGGGKLLAAHVIOILVIAGVNSATMGPLFWGLNKLK-LRISSEDELAG 460
 DB 424 -----GLFYGGINQLIIQIVGILAI-GAFTAFSVVMAILKQTWGIKRVSGEEMIG 475
 QY 461 MDNTHGGFAYAYEDDETHKHG 482
 DB 476 LDIGEHEMAYTGFVKETDSFG 497

RESULT 10

YAL7 SYN3
 ID YAL7 SYN3 STANDARD; PRT; 442 AA.
 AC P72935;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Putative ammonium transporter sll1017.
 SN SLL1017.
 SS Synchocystis sp. (strain PCC 6803).
 SC Bacteria; Cyanobacteria; Chroococcales; Synchocystis.
 SX NCBI_TaxID=1148;
 SN SLL1017.
 RP SEQUENCE FROM N.A.
 MEDLINE=97061201; PubMed=8905231;
 RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
 RA Miyajima N., Hirose M., Sugita M., Saito S., Kimura T.,
 RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
 RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
 RA Yamada M., Yasuda M., Tabata S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synchocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-135(1996).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49)
 CC family.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; D90901; BAA16952.1; --
 CC PIR; S74801; S74801.
 CC InterPro; IPR001905; Ammonium transp.

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DR InterPro; IPR002229; RhesusRD.  
DR Pfam; PF00909; Ammonium transp; 1.  
DR PRINTS; PRO0342; RHEUSRD.  
DR TIGRFAMs; TIGR00836; amt; 1.  
DR PROSITE; PS01219; AMMONIUM TRANSP; 1.  
KW Hypothetical protein; Transport; Transmembrane; Complete proteome.  
FT TRANSMEM 5 25 POTENTIAL.  
FT TRANSMEM 44 64 POTENTIAL.  
FT TRANSMEM 81 101 POTENTIAL.  
FT TRANSMEM 104 124 POTENTIAL.  
FT TRANSMEM 133 153 POTENTIAL.  
FT TRANSMEM 155 175 POTENTIAL.  
FT TRANSMEM 193 213 POTENTIAL.  
FT TRANSMEM 240 260 POTENTIAL.  
FT TRANSMEM 269 289 POTENTIAL.  
FT TRANSMEM 299 319 POTENTIAL.  
FT TRANSMEM 325 345 POTENTIAL.  
FT TRANSMEM 354 374 POTENTIAL.  
FT TRANSMEM 386 406 POTENTIAL.  
SQ SEQUENCE 442 AA; 47172 MW; F3683BF23D96539E CRC64;  
  
Query Match 25.7%; Score 678.5; DB 1; Length 442;  
Best Local Similarity 35.9%; Pred. No. 2.5e-40;  
Matches 168; Conservative 61; Mismatches 152; Indels 87; Gaps 15;  
  
2y 38 SKFVDTAFADVNTYLLFSAYLVFSMOLGFAMLCAGSVRAKNTNMIMLTNVLDAAGGLFY 97  
3b 32 TSAEVTYAINFLAAVLVFMAGFAMLEAGLSHSHNTVNVLFKNTPTVCVGVLLY 91  
2y 98 YLGFAPAFAGSPS--NGFICKHFG----LKDIPSSSYDYSLYQWAFAPAAAGITSGS 151  
3b 92 FLFGSLMYGENPVLGGFFGCGGFGITNLDNVEGLSPQVDW-LFOAAPAAATAATVSGA 150  
2y 152 IABRTQVAVLYSSFLTPVPSVSHWFSPDGWSAFKIDTRLFSTGVIDFAGSGVVH 211  
3b 151 VMGRMYFAVLYTSVAVITGLVPIGSHRWG-GGW-----LDKL---GFHDFAGSLVH 200  
2y 212 MYGGIAGLWGLTEGPRMGRFDHAGRAVALRGH----SASLVVLTGLFLWFGYFNFGS 267  
3b 201 SVGGFAALAAVVMGPRIGRFE--GNKINSLGYQGITSSS---LGVFILWGVWGFNFGS 255  
2y 268 FNKILLYGNNGNYGQWSAVGR-----TAVTTLAGSTPAALTTLGKRVISGHW--- 317  
3b 256 -----QLAFVGAINTNTTMLIAVNTLSAAAGGLAAL-----AFDMIT 293  
2y 318 -----NVDVNCGLLGFAAATAGCSVVEPMAAIVCGFVASIVLACNKLAEKVKFDDP 371  
3b 294 ENKEKPNLLVTLNGLGLVGTAGCDTVSNWSAIALGVVAGILSVLGTKLDRLRIDG 353  
2y 372 LEAQLHGGCGTGWVIFTALPAKKEVYKVEYVGLGRAHGLMGGGGKLLAAHVQILVIAG 431  
3b 354 VGAWPVEGLCGINGGIAVGIFSTNVEHK-----LSAQVGLSLVTFP 394  
2y 432 WVSATMGPLFWGLNKLKLRISSSEDELAGMDMTRHG----GPAAYED 475  
3b 395 WAFITMFEFLFVMDLWGLLRKPSQEKVGLDIVEHGQTEKGVIEIAPED 442  
  
RESULT 11  
AMT3 CAEEL  
ID AMT3 CAEEL STANDARD; PRT; 687 AA.  
AC Q21565;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Putative ammonium transporter amt-3.  
GN AMT-3 OR M195.3.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI_TaxID=6239;  
RN (1)  
RP SEQUENCE FROM N.A.
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RC STRAIN=Bristol N2;  
RA Burton J.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP REVISIONS.  
RA Durbin R.; (DEC-2002) to the EMBL/GenBank/DBJ databases.  
RL Submitted;  
CC -!- FUNCTION: Involved in the uptake of ammonia (probable).  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (probable).  
CC -!- SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49)  
family.  
CC  
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CC or send an email to license@ebi.ac.uk).  
CC  
CC EMBL; Z66498; CAA91293.2; -;  
DR PIR; T23804; T23804.  
DR WormPep; M195.3; CE32912.  
DR InterPro; IPR001905; Ammonium transp.  
DR Pfam; PF00909; Ammonium transp; 1.  
DR TIGRFAMs; TIGR00836; amt; 1.  
DR PROSITE; PS01219; AMMONIUM TRANSP; 1.  
KW Hypothetical protein; Transport; Transmembrane.  
FT TRANSMEM 35 59 POTENTIAL.  
FT TRANSMEM 77 97 POTENTIAL.  
FT TRANSMEM 134 154 POTENTIAL.  
FT TRANSMEM 162 182 POTENTIAL.  
FT TRANSMEM 196 216 POTENTIAL.  
FT TRANSMEM 240 260 POTENTIAL.  
FT TRANSMEM 272 292 POTENTIAL.  
FT TRANSMEM 299 319 POTENTIAL.  
FT TRANSMEM 323 343 POTENTIAL.  
FT TRANSMEM 352 372 POTENTIAL.  
FT TRANSMEM 404 424 POTENTIAL.  
SQ SEQUENCE 687 AA; 73937 MW; 90BA97A928918E01 CRC64;  
  
Query Match 22.0%; Score 579.5; DB 1; Length 687;  
Best Local Similarity 31.8%; Pred. No. 3.2e-33;  
Matches 156; Conservative 86; Mismatches 163; Indels 79; Gaps 19;  
  
Qy 14 LLGPNTT--DASAAASLIQGHFAVD-SKFVDTPAFVNDTYLLFSAYLVFSMOLGFAMLC 70  
Db 1 MAGPEGSIFNASAMQIVQIHVYAGSVTPVDKLYQDDAVWISSSFIIFTHSGFGILE 60  
Qy 71 AGSVRAKNTNMIMLTNVLDAAGGLFYILFGFAFAG-----SPSNGFICKHF----- 118  
Db 61 SGVSARDEVNIMRVNDVDFVFGLSYWSCGFGFSYGDIPWRNPYVGF-GRFYDPTRD 119  
Qy 119 FGLKD-IPSSSYDYSLYQWAFAPAAAGITSGSIAERTQFVAYLYSSFLTGFVYPVVS 177  
Db 120 YGTRETNQEGSYASFLQLSLATTASTIVSGAVERAKLSYLLGCVI-LIQALPA 178  
Qy 178 HFWSPDQWASAFKIDTRLFSTGVIDFAGSGVHVMVGGIAGLWGLTEGPRMGRFDHAGR 237  
Db 179 HWYMDKEG-----VFYKKGVDVDFAGCSAVHLVGGIIGLIATVFLKPRRNFNEDS- 228  
Qy 238 AVALRGHSASLVLTGLTFWFGVFNPGSNFKILLTYGNSGNYGQWSAVGRTAVTTTL 297  
Db 229 --VHQMSSPTNALLGTLFWGFWGINAGS-----VWGITG---GRNGLGARAATIM 277  
Qy 298 A---GSTAALTTLFGKRVISGHWNVTDVNCGLLGGFAAITAGCSVVEPMAAIVCGFVASI 354  
Db 278 ASIGGGATATTSFVK---TKLQVNFNLINGLSSITSITAI CAVSRPWHALVIGSISV 334  
Qy 355 VLIACNKLAEKVKFDDPLEAAQLHGGCGTGWVIFTALPAKKEVYKVEYVGLGRA-----HGL 410  
Db 335 FSIATVPLDLRLHIDDPVIGIVFIHLTSSIWGVIAGVIFCEEKY-----LGSATNRSGL 389
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2Y 411 LMGGGKLLAAHVQIYIAGWV-----SATMPL-FWGLNKLKL-LRISSEDE 457
2b 390 LYSWSPFELL-----WVQLQTAAILIYSATTGFLALFLISKSPGLRAVTDYEE 437
2Y 458 LAGMDVTRHG 467
2b 438 QIGADVIEHG 447

RESULT 12
(537 SYNY3
ID Y537 SYNY3 STANDARD; PRT; 541 AA.
AC P44148;
JT 01-OCT-1996 (Rel. 34, Created)
JT 01-OCT-1996 (Rel. 34, Last sequence update)
JT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative ammonium transporter s110537.
ZN S110537.
DS Synechocystis sp. (strain PCC 6803).
DC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
DX NCBI_TaxID=1148;
ZN [1]
SEQUENCE FROM N.A.
MEDLINE=96127529; PubMed=850279;
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugiyama M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome."
RL DNA Res. 2:153-166(1995).
TC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
TC -1- SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49)
TC family.
TC -----
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TC -----
TC EMBL; D64006; BAA10864.1; --
TC PIR; S76017; S76017.
TC InterPro; IPR001905; Ammonium_transpt.
TC Pfam; PF00909; Ammonium_transp; 1.
TC SMART; SM00304; HAMP; 1.
TC TIGRfam; TIGR00836; ant; 1.
TC PROSITE; PS01219; AMMONIUM_TRANS; 1.
TC Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 6 26 POTENTIAL.
FT TRANSMEM 44 64 POTENTIAL.
FT TRANSMEM 86 106 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 161 181 POTENTIAL.
FT TRANSMEM 203 223 POTENTIAL.
FT TRANSMEM 235 255 POTENTIAL.
FT TRANSMEM 260 280 POTENTIAL.
FT TRANSMEM 283 303 POTENTIAL.
FT TRANSMEM 316 336 POTENTIAL.
FT TRANSMEM 356 376 POTENTIAL.
SQ SEQUENCE 541 AA; 58129 MW; A7A0A5CB2FFD2475 CRC64;

Query Match 21.6%; Score 569.5; DB 1; Length 541;
Best Local Similarity 33.2%; Pred. No. 1.3e-32;
Matches 153; Conservative 58; Mismatches 191; Indels 59; Gaps 12;

2Y 46 ADVNTYLLFSAIYVFSMQLGFMALCAGSVAKNTMIMLTNVLDAAGGLFYLFQFAFA 105
2b 3 SIDTLWLLLCAGLVFFVQAGFMCLSGLTRSKNSINVAIKNFPADGISVALFWSFGFSIM 62
2Y 106 FGSPSNGFIHGHHFGLKIDIFSSSYDYSYFLYQWAFIAAAGITSGSIARTQFVAYLIYS 165

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Db 63 FGLSGGWMGTG-YSFVDVGGEPTLAVFFLFQAMFCGTATTISGAABERKFSAYLLVA 121
QY 166 SPLTGFPVVPVSHVFW-----SPDQWASAFKITDRLFSTGVIDFAGSGVHMVVG 215
Db 122 GLASGLIYPLFGDMAWGLATVAGIETGGW-----LENLGRDFAGSTVWHSVGA 172
QY 216 IAGLWGLIEGPRGRPDHAGRAVALRHSASLVVGLTFLFWGTYGPNFGSPFNKILTY 275
Db 173 WIGLATIIVWGPGRFPKTKIKQGSNNPFSVLGTLLFWGLGFGNGS-----TF 226
QY 276 GNSGNYQWMSAVGRTAVTTTLAG-----STAALTTLFGKEVISHWNVTVDVNCGLLG 331
Db 227 GLTPEVPG-----IMVNTVLAVGGMLMAGLSLQDKMI-----QVEPLMNGSLAGLV 275
QY 332 AITAGCSVVEFWAALVCGFVASIVLIACNKLAEKVPDPLEAAQLHGGCGTGWVIFTAL 391
Db 276 AITASANYVTMTPIAMVIGATSAIYLVGKKMLHWGVDDAVAVHGGVAGVGTJCVGL 335
QY 392 FAKKEYVKEVYGLGRHGLLMGGGKLLAAHVQIYIAGWV-----GWVSATMGLFWGLNKLKL 450
Db 336 FQQLPLVDT--GLNRWQC-----GVQLLGIGVCTLWAFGLAWVFLTL-----LNRVFA 383
QY 451 RISSDELAGMDMTRHGGFAVAYE-----DDETHKGMQLR 486
Db 384 RISPSDEBIGLVNVEHQATTETTYELFQVMDRQAKTHDLSLR 424

RESULT 13
AMT_MYCTU
ID AMT_MYCTU STANDARD; PRT; 477 AA.
AC Q10968;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable ammonium transporter.
GN AMT OR RV2220C OR M2988 OR M2C338.09C OR MB2944C.
OS Mycobacterium tuberculosis, and
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773, 1765;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=H37Rv;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekoaia F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RL complete genome sequence."
RL Nature 393:537-544(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RX MEDLINE=22206494; PubMed=12218036;
RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Doolittle A., Uitterlinden T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.bovis; STRAIN=AF2122/97;
RX MEDLINE=22709107; PubMed=12788972;

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RA Garnier T., Eigelmeier K., Camus J.-C., Medina N., Mansoor H.,
 RA Pryor M., Duchoy S., Grondin S., Lacroix C., Monsemp C., Simon S.,
 RA Harris B., Ackin R., Doggett J., Maves R., Keating L., Wheeler P.R.,
 RA Parkhill J., Barrell B.G., Cole S.T., Gordon S.V., Hewinson R.G.,
 RA "The complete genome sequence of Mycobacterium bovis.",
 RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882(2003).
 CC -!- FUNCTION: Involved in the uptake of ammonia (Probable).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -!- SIMILARITY: Belongs to the ammonium transporter (TC 2.A.49)
 CC family.
 CC
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 CC
 DR EMBL; Z74697; CAA98980.1; -;
 DR EMBL; AE007120; AAK47314.1; -;
 DR EMBL; BX248344; CAD96631.1; -;
 DR PIR; H70747; H70747.
 DR TIGR; MT2988; -;
 DR TubercuList; RV2920C; -;
 DR InterPro; IPR001905; Ammonium_transp.
 DR Pfam; PF00909; Ammonium_transp; 1.
 DR TIGRFAMs; TIGR00836; amn; 1.
 DR PROSITE; PS01219; AMMONIUM_TRANSP; 1.
 KW Transport; Transmembrane; Complete proteome.
 FT TRANSMEM 16 36
 FT TRANSMEM 53 73
 FT TRANSMEM 121 141
 FT TRANSMEM 150 170
 FT TRANSMEM 192 212
 FT TRANSMEM 229 249
 FT TRANSMEM 257 277
 FT TRANSMEM 290 310
 FT TRANSMEM 312 332
 FT TRANSMEM 344 364
 FT TRANSMEM 394 414
 FT TRANSMEM 477 494; 49241 MW; 97CB46A1C1063DFE CRC64; -;
 SQ SEQUENCE 477 AA; 18%; Score 496; DB 1; Length 477;
 Query Match
 Best Local Similarity 29.7%; Pred. No. 1.5e-27;
 Matches 146; Conservative 79; Mismatches 195; Indels 72; Gaps 17;
 QY 48 DNTVLLPSAYLVFSPQGLGFMALCAGSVRAKNTWMLTNVLDAAAGLFYLLGPAFAFG 107
 DB 14 DTAWLVSSALVLLMTPLGLAFYFGWVRKSVLNMNMISAMGVTVTLWALYGYSIAGF 73
 QY 108 SPNSNGFIG--KHFFGLK-----DIP-SSSYDYSYFL-YQWAFIAAA 144
 DB 74 DDVGNIAQNPQYGLKGLIGNVAAADPSTQTAAVNIPLAGTLPATVFAQLMPAIIIT 133
 QY 145 AGITSGSIAERTQFVAVLIYSFTGFVYVSHFWSPGWSAKK--ITDRLPSTGVI 202
 DB 134 VALISGAVADRLKFGAMLLFAGLWATTFYFPVAHWFAFDGFAERGGMIANKLHA---I 190
 QY 203 DFAGSGVHWVGGLAGLWGLALIEGRMGREFDHAGRAVALRGHSLVLTGLTFLLPWGTYG 262
 DB 191 DFAGTAVHINAGVAALMLAIVLGRKG-----WPATLFPNHLFPVLMGAALLNFGWYG 245
 QY 263 FNPGSFNKILTYGNSGNYGQWSAVGRTAVTTLAGSTAALTTLFGKRVISGHMNVTV 322
 DB 246 FNAGS-----ATTAN-----GVAGATFTVTTTATAAAMGLWLLTERVRDGGKATTLGA 292
 QY 323 CNGLLGGFAATACGSVVEPWAAIVCCGFVASIVLIACNKLAEKVKDDPDLAAQLHGCGG 382
 DB 293 ASGIVAGVAVLTPSCSSVNVLCALAVGSAGVLCALAVGLKFKLGGFDDSLDVVGVLVGG 352
 QY 383 TWGVITTFALFAKKEVYKEVYGL-GRAGHLLMGCGGKLL---AAHFVQILVIAGWSATMG 438

Db 353 LVGTLVLGLAAPE-APAINGVAGVSKGLFYGGGPAQLRQALGACSVLVYSGIITILA 411
 QY 439 PLFWGLNKLKLL--LRISSEDELAGMDTRH--GGFAYAYEDD-----ETHKHGMQ 484
 Db 412 LI-----LKFIFGLRLDAEQSTGIDEAEHAESGYDFAVASGSLVPRVTVEDSRNGIQ 465
 QY 485 LRRVGNASSTP 496
 Db 466 -ERIGQKVEAEP 476
 RESULT 14
 NRGABACSU STANDARD; PRT; 404 AA.
 AC Q07429;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DB Probable ammonium transporter (Membrane protein nrga).
 GN NRGABACSU36510.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94110214; PubMed=8282685;
 RA Wray L.V. Jr., Atkinson M.R., Fisher S.H.;
 RT "The nitrogen-regulated Bacillus subtilis nrgAB operon encodes a
 RT membrane protein and a protein highly similar to the Escherichia coli
 RT glnB-encoded PII protein.";
 RL J. Bacteriol. 176:1108-1114(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RA MEDLINE=96015417; PubMed=9353933;
 RA Presecan E., Moszer I., Boursier L., Cruz Ramos H.C., De La Fuente V.,
 RA Hullo M.-F., Lelong C., Schleich S., Sekowska A., Song B.H.,
 RA Villani G., Kunst F., Danchin A., Glaser P.;
 RT "The Bacillus subtilis genome from gerBC (311 degrees) to licker (334
 RT degrees).";
 RL Microbiology 143:3313-3328(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX STRAIN=168;
 RA MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Haelech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Paro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Fujic C., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Taccori E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tanakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vanier F., Vassarotti A.,
 RA Viari A., Wambut R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,

Db 61 KKNVNNVMMKXVNDWLGCVAWLPIGGILCSKGFDLISAFIDWKKQILG-TNWFNGLDLA 119
Qy 133 YFLYQWAFALAAAGITSGTAERTQFVAYLIYSFLTGFVVPV---VSHWFWSFGWASA 189
Db 120 SWFFGLVFCATAATIVSGGVAERIKFSAYVLI SLIITGLDYLPLFVYLGFWGASIVFWH-- 177
Qy 190 PKITDRLFTGVIDFAGSGVVMVGGIAGLWGALIEGPRMGRPDHAGRAVALRGHSASLV 249
Db 178 -----DYAGSLVHGLGGFLALGATAALGPRIGRFVD-GRPVPILGHNIPMA 223
Qy 250 VLGTPELLWFGWYGNPQSFNKKILTYGNSGNYGQWSAVGRTAVTTTLAGSTAALTTLFG 309
Db 224 VFGAFALAIGWYGNFVGS-----SLALGDIS-----GLVCAITTMVAGGGIGALIA 270
Qy 310 KRVISGHNVTDCNGLLGGFAAITAGCSVVEPWAAIVCGFVASIVLIACNKLAEKVKFD 369
Db 271 SRN-----DVLFTANGIVAGLVAICSTDVVSPIGGLIIGLIAGLOVPVYKLVKAGLD 325
Qy 370 DPLEAAQLHGGCGTWGVIPTALPAKKEYVKEVYGLGRAHGLLMGGGKLLAAHVQIL-- 427
Db 326 DVCGVVPVHGTAGVIGAILTGILGK-----IFG-----GAGGVSLLIDQIIGAVFC 371
Qy 428 -----VIAGVVSATMGPLFWGLNKLKLLRISSEDELAGMDMTRHGGFAYAYE 474
Db 372 ILYGTGLGYILLAKIVGIALGG-----LRVSEEEKXGGLDMAEHKMPAYPEE 417

Search completed: March 9, 2004, 11:54:37
Job time : 20 secs

Result	No.	Score	Query	Match	Length	DB	ID	Description
1	254	5	85	4	501	10	Q9FV14	locus japon
2	249	5	85	2	502	10	Q3FSH3	locus japon
3	2001	75	8		518	10	Q71IB9	locus japon
4	1995	75	6		519	10	Q3FUH7	brassicaceae
5	1988	75	4		496	10	Q3CLK1	arabidopsids
6	1962	74	3		498	10	Q7XQ12	oryza sativ
7	1960	74	3		532	10	Q947N1	oryza sativ
8	1840	75	6		495	10	Q947M9	oryza sativ
9	1792	75	6		533	10	Q04400	oryza sativ
10	1655	75	6		497	10	Q947N0	oryza sativ
11	1463	55	4		335	10	Q3ZPN8	nepenthes a
12	1089	5	41	3	579	10	Q3LRM5	chlamydomon
13	1087	5	41	2	579	10	Q3LRM4	chlamydomon
14	1078	40	8	3	539	10	Q8RUT6	chlamydomon
15	968	36	7	3	542	10	Q81JU0	chlamydomon
16	921	34	9	1	511	10	Q94K17	cylindrothe

QY 61 SMQLGFAMLCAGSVRAKNTNIMLTNVLDAAGGLFYLLFGFAFAFGSPSNGFIGKHFPG 120
 Db 61 SMQLGFAMLCAGSVRAKNTNIMLTNVLDAAGGLFYLLFGFAFAFGSPSNGFIGKHFPG 120
 QY 121 LKDPSSSYDYSFLYQWAFAPAIAGAGITSGSIAERTQFVAYLIYSSFLTGFPVYVSHWF 180
 Db 121 LKDPVTFADYSFLYQWAFAPAIAGAGITSGSIAERTQFVAYLIYSSFLTGFPVYVSHWF 180
 QY 181 WSPGWSAFKIDRLFLSTGVIDFAGSGVVMVGGIAGLWGLALIEGPRMGRFDHAGRAVA 240
 Db 181 WSGGWSATNTGNLLFGTGVDFAGSGVVMVGGIAGLWGLALIEGPRMGRFDHAGRAVA 240
 QY 241 LRHSASLVLTGTFLLWFGYGNFPGSNFKILLITYGNSGNYGQWSAVGRTAVTTTLGAGS 300
 Db 241 LRHSASLVLTGTFLLWFGYGNFPGSNFKILLITYGNSGNYGQWSAVGRTAVTTTLGAGS 300
 QY 301 TAAATTTLFGKRVISGHNVTDVNCGLLGGAFAAITAGCSVVEPAAIIVCGFVASIVLIACN 360
 Db 300 TAAATTTLFGKRVISGHNVTDVNCGLLGGAFAAITAGCSVVEPAAIIVCGFVASIVLIACN 360
 QY 361 KLAEKVFPDDPLEAAQLHGGCGTGWVIFTALFAKKEVYKEVY--GLGRAHGLLMGGGGKL 418
 Db 360 MLEAKVRYDDPLEAAQLHGGCGTGWVIFTALFAKKEVYVQVYVPGKGRPYGLFMGGGGKL 419
 QY 419 LAAHVQILVITAGVNSATMGPLFWGLNKLKLRISSEDELAGMDTRHGGFAVAYEDDET 478
 Db 420 LGARVQILVITAGVNSATMGPLFWGLNKLKLRISSEDELAGMDTRHGGFAVAYEDDES 479
 QY 479 HKGQQLRRVGNPNASSTPTTD 499
 Db 480 HKPGIQLRKIEPNSSSTPSAE 500

RESULT 2

Q9FSH3 ID Q9FSH3 PRELIMINARY; PRT; 502 AA.
 AC Q9FSH3;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Ammonium transporter (AMT1.1).
 GN AMT1.1.
 OS Lotus japonicus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
 CX NCBI_TaxID=34305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21297198; PubMed=11404021;
 RA Salvemini F., Marini AM., Riccio A., Patriarca E.J., Chiurazzi M.;
 RT "Isolation of a member of the Lotus japonicus AMT1 family."
 RL Gene 270:237-243(2001).
 DR EMBL; AJ279059; CAC10555.1; -;
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008519; F:ammonium transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001905; Ammonium transp.
 DR InterPro; IPR01064; Crystallin.
 DR Pfam; PF00909; Ammonium transp; 1.
 DR TIGRFam; TIGR00836; amT; 1.
 DR PROSITE; PS01219; AMMONIUM_TRANS; 1.
 DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
 DR SEQUENCE 502 AA; 53395 MW; BE65AB790668159B CRC64;

Query Match 85.2%; Score 2249.5; DB 10; Length 502;
 Best Local Similarity 84.0%; Pred. No. 8.7e-152;
 Matches 420; Conservative 38; Mismatches 39; Indels 3; Gaps 2;

QY 2 SLPACPAEQIAQLLGPNTDASAAASLTCGHFAAVDSKFVDTPAFVNTYLLFSAYLVFS 61
 Db 3 ALPECSAANLAQLIGNATDAAVAGFICDQFTAVGQRFSDTAFVNTYLLFSAYLVFS 62

QY 62 MQLGPFAMLCAGSVRAKNTNIMLTNVLDAAGGLFYLLFGFAFAFGSPSNGFIGKHFPG 121
 Db 63 MQLGPFAMLCAGSVRAKNTNIMLTNVLDAAGGLFYLLFGFAFAFGSPSNGFIGKHFPG 122
 QY 122 KDPSSSYDYSFLYQWAFAPAIAGAGITSGSIAERTQFVAYLIYSSFLTGFPVYVSHWF 181
 Db 123 KDPVTFADYSFLYQWAFAPAIAGAGITSGSIAERTQFVAYLIYSSFLTGFPVYVSHWF 182
 QY 182 SPGWSAFKIDRLFLSTGVIDFAGSGVVMVGGIAGLWGLALIEGPRMGRFDHAGRAVA 241
 Db 183 SGGWSATNTGNLLFGTGVDFAGSGVVMVGGIAGLWGLALIEGPRMGRFDHAGRAVA 242
 QY 242 RGHASLVLTGTFLLWFGYGNFPGSNFKILLITYGNSGNYGQWSAVGRTAVTTTLGAGS 301
 Db 243 RGHASLVLTGTFLLWFGYGNFPGSNFKILLITYGNSGNYGQWSAVGRTAVTTTLGAGS 301
 QY 302 AATTTLFGKRVISGHNVTDVNCGLLGGAFAAITAGCSVVEPAAIIVCGFVASIVLIACN 361
 Db 302 AATTTLFGKRVISGHNVTDVNCGLLGGAFAAITAGCSVVEPAAIIVCGFVASIVLIACN 361
 QY 362 LABKVPDDPLEAAQLHGGCGTGWVIFTALFAKKEVYKEVY--GLGRAHGLLMGGGGKL 419
 Db 362 LABKRVYDDPLEAAQLHGGCGTGWVIFTALFAKKEVYVQVYVPGKGRPYGLFMGGGGKL 421
 QY 420 AAHVQILVITAGVNSATMGPLFWGLNKLKLRISSEDELAGMDTRHGGFAVAYEDDET 479
 Db 422 GAHVQILVITAGVNSATMGPLFWGLNKLKLRISSEDELAGMDTRHGGFAVAYEDDES 481
 QY 480 HKGQQLRRVGNPNASSTPTTD 499
 Db 482 KPGIQLRKIEPNSSSTPSAE 501

RESULT 3

Q7YIB9 ID Q7YIB9 PRELIMINARY; PRT; 518 AA.
 AC Q7YIB9;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ammonium transporter.
 GN AMT1.2.
 OS Lotus japonicus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Lotaeae; Lotus.
 CX NCBI_TaxID=34305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA El Alsouli H., Chiurazzi M.;
 RT "Characterization of a new ammonium transporter in Lotus japonicus."
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY135020; AAM95453.1; -;
 DR SEQUENCE 518 AA; 54830 MW; BE55526F051055C0 CRC64;

Query Match 75.8%; Score 2001; DB 10; Length 518;
 Best Local Similarity 75.8%; Pred. No. 4.2e-134;
 Matches 383; Conservative 41; Mismatches 73; Indels 8; Gaps 5;

QY 1 MSLPACPAEQIAQLLGPNTDASAAASLTCGHFAAVDSKFVDTPAFVNTYLLFSAYLV 59
 Db 1 MASLSCSATDLAPLLTATTNATATAATVLCNQLDTISRKLSDTTAVDNTYLLFSAYLV 60
 QY 60 FSQLGPFAMLCAGSVRAKNTNIMLTNVLDAAGGLFYLLFGFAFAFGSPSNGFIGKHFPG 119
 Db 61 FAMQLGPFAMLCAGSVRAKNTNIMLTNVLDAAGGLFYLLFGFAFAFGSPSNGFIGKHFPG 120
 QY 120 GLKDPSSSYDYSFLYQWAFAPAIAGAGITSGSIAERTQFVAYLIYSSFLTGFPVYVSHW 179
 Db 121 GLKHPSTYDYSFLYQWAFAPAIAGAGITSGSIAERTQFVAYLIYSSFLTGFPVYVSHW 180
 QY 180 FWSPDGNWASAFKIT-DRLFSTGVDFAGSGVVMVGGIAGLWGLALIEGPRMGRFDHAGRA 238

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Db 181 LWSDDWASPRTRTGSLLPGSAGIDFAGSGVHVHVGAGIAGWAFEGPRIGRFORIGERS 240
Qy 239 VALRGHSASLVLTGFTLLWGTGWFNPGSNKILLTVGN---SGNYVGOWSAVGRFAVTT 295
Db 241 VALRGHSASLVJLSFLWFGWGFNPGSFLTTAKAYGNGENGNTYIGOWSAIGRFAVTT 300
Qy 296 TLASTAALTTLFQKRVISGHWNVTVCNGLLGGFAAITAGCSVWPWAAIIVCGFVASIV 355
Db 301 TLAGCTAALTTLFQKRVISGHWNVTVCNGLLGGFAAITAGCSVWPWAAIIVCGFVASIV 360
Qy 356 LIACNKLAEVKVFDPLEAQLHGGCGTGWVIFTALFAKKEVYKVEYGL--LGRAHGLMGG 414
Db 361 LIGLNLVAARKVDDPLEAQLHGGCGGAGVLTGLFAKGEYVAEYVGSAGRPYGLLMGG 420
Qy 415 GKKLLAAHVIQILVIAGVSVATMGPLFWGLNKLKLLRISSSEDELAGMDTREGGFAYAYE 474
Db 421 GKKLLAAQVIBILVVCVWVTATMGPLFWGLNKLKLLRISSSEDELAGMDTREGGFAYAYH 480
Qy 475 DDE--THKGNGQLRRVGNASSTPT 497
Db 481 DDDVSTKRGVMSRIGFGSSSPST 505

RESULT 4
Q9FUH7 PRELIMINARY; PRT; 519 AA.
AC Q9FUH7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE High-affinity ammonium transporter AWT1,2.
OS Brassica napus (Rape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3708;
RN [1]
RP SEQUENCE FROM N.A.
RA Pearson J.N., Finnemann J., Schioerring J.K.;
RT "Regulation of the high-affinity ammonium transporter (BnAMT1;2) in
RL the leaves of Brassica napus by nitrogen status.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF306518; AAG28780.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008519; F:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium_transpt.
DR Pfam; PF00909; Ammonium_transp; 1.
DR TIGRFAMs; TIGR00836; amt; 1.
DR PROSITE; PS01219; AMMONIUM_TRANS; 1.
SQ SEQUENCE 519 AA; 55759 MW; 2F30322B1A146D4E CRC64;

Query Match 75.6%; Score 1995; DB 10; Length 519;
Best Local Similarity 77.1%; Pred. No. 1.1e-133;
Matches 378; Conservative 36; Mismatches 62; Indels 12; Gaps 5;

Qy 6 CPAEQLAQLGPNNTDASAAALICGHFAAVDSKFDVDTAFADVNTYLLFSAYLVFSMQLG 65
Db 7 CSAADLATLLGN---ATAADYICGQLGVNKNFTDAAFIDNTYLLFSAYLVFAMQLG 63
Qy 66 FAMLCAGSVRANKTNMILTNVLDAAAGGLFYFLFGFAFGSPSGNGFIKHFGLKDIP 125
Db 64 FAMLCAGSVRANKTNMILTNVLDAAAGGLFYFLFGFAFGSGSEGFGRNFAIRDFP 123
Qy 126 SSSYDYSFYLQWAFAPAAAGITSGSIAERTQFVAVLYSSFLTGFPVYVSWHFWSPDG 185
Db 124 TPTADYSFYLQWAFAPAAAGITSGSIAERTQFVAVLYSSFLTGFPVYVSWHFWSPDG 183
Qy 186 WASAFK-ITDELFTGVIDFAGSGVHVHVGAGIAGWAFEGPRIGRFORIGERS 244
Db 184 WASPFRSADRLFTGVIDFAGSGVHVHVGAGIAGWAFEGPRIGRFORIGERS 243
Qy 245 SASLVLTGFTLLWGTGWFNPGSNKILLTVGN---SGNYVGOWSAVGRFAVTT 304
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Db 244 SASLVLTGFTLLWGTGWFNPGSNKILLTVPY-NSGNTYGVGSGIGRTAVNTLSGCTAAL 302
Qy 305 TTLFGKRVISGHWNVTVCNGLLGGFAAITAGCSVWPWAAIIVCGFVASIVLIACNKLAE 364
Db 303 TTLFGKRVISGHWNVTVCNGLLGGFAAITAGCSVWPWAAIIVCGFMTSLVLIGCNKLAE 362
Qy 365 KVAFDDPLEAQAQLHGGCGTGWVIFTALFAKKEVYKVEYGL--GRAHGLMGGGGKLLAAH 422
Db 363 LVQYGDPLEAQAQLHGGCGAGVLTGLFAKKEVYKVEYGLFGVGLFMGGGGKLLGAQ 422
Qy 423 VIQILVIAGVSVATMGPLFWGLNKLKLLRISSSEDELAGMDTREGGFAYAYEDDTHKG 482
Db 423 LVQILVIAGVSVATMGPLFWGLNKLKLLRISSSEDELAGMDTREGGFAYAYEDDTHKG 481
Qy 483 MQLRRVGPNA 492
Db 482 ---RVDPGS 487

RESULT 5
Q9LK16 PRELIMINARY; PRT; 496 AA.
AC Q9LK16;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ammonium transporter.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RX MEDLINE=20363099; PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones.";
RL DNA Res. 7:217-221(2000).
DR EMBL; AP000382; BAB02928.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008519; F:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium_transpt.
DR Pfam; PF00909; Ammonium_transp; 1.
DR TIGRFAMs; TIGR00836; amt; 1.
DR PROSITE; PS01219; AMMONIUM_TRANS; 1.
SQ SEQUENCE 496 AA; 52638 MW; FB97C38A94D17B5B CRC64;

Query Match 75.4%; Score 1988.5; DB 10; Length 496;
Best Local Similarity 76.1%; Pred. No. 3.1e-133;
Matches 375; Conservative 46; Mismatches 65; Indels 7; Gaps 4;

Qy 6 CPAEQLAQLGPNNTDASAAALICGHFAAVDSKFDVDTAFADVNTYLLFSAYLVFSMQLG 65
Db 7 CSAADLATLLGN---ATAADYICGQLGVNKNFTDAAFIDNTYLLFSAYLVFAMQLG 63
Qy 66 FAMLCAGSVRANKTNMILTNVLDAAAGGLFYFLFGFAFGSPSGNGFIKHFGLKDIP 125
Db 64 FAMLCAGSVRANKTNMILTNVLDAAAGGLFYFLFGFAFGSGSEGFGRNFAIRDFP 123
Qy 126 SSSYDYSFYLQWAFAPAAAGITSGSIAERTQFVAVLYSSFLTGFPVYVSWHFWSPDG 185
Db 124 TLTSDYSFYLQWAFAPAAAGITSGSIAERTQFVAVLYSSFLTGFPVYVSWHFWSPDG 183
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QY 242 RGHASLWLTGTLFWGNGFNPSPFNKILLTYGNSGNYGOWSAVGRVAVTTTLAGST 301
Db 230 KGHASLWLTGTLFWGNGFNPSPFNKILLTYGNGSNGVGRVAVTTTLAGSV 289
QY 302 AALTTLFGKRVISGHNVNVDVCGNLGGFAATAGCGSVVEPMAIIVCGFVASIVLIACNK 361
Db 290 AALTTLFGKRLQTHNVNVDVCGNLGGFAATAGCGSVVDPMAIICGVFSAWLIGLNA 349
QY 362 LAEKVYDDPLEAAQLHGGCGTGWVIFTALFAKKEVYKVEYGLGRAHGLLMGGGKLAA 421
Db 350 LAELKEDDPLEAAQLHGGCGAGILFTALFAKQVVEHLYGAGRPYGLFMGGGKLAA 409
QY 422 HVIQILVAGVSTAGTGLFWGLNKLKLRISSDELACMDMTRHGGFAYAYEDDETHKH 481
Db 410 HVIQILVIFGVNCTMGFLFVGLKGLLRISAEDETSGMDLTHRGGFAYVYVHDEHDK 469
QY 482 ---GMQLR---RVGNAS 493
Db 470 SGVGFMLRSQTRVEPAAA 489

RESULT 8
ID Q947M9 PRELIMINARY; PRT; 495 AA.
AC Q947M9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ammonium transporter 1-3.
GN OSAMT1.3.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Hoque M.S., Masle J., Udvardi M.K., Upadhyaya N.M.;
RT "Cloning and characterization of three Ammonium transporter genes from
RT rice.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF289479; AAL05614.1; -.
DR Gramene; Q947M9; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008519; P:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium transp.
DR Pfam; PF00909; Ammonium transp; 1.
DR TIGRFAMs; TIGR00836; amt; 1.
SQ SEQUENCE 495 AA; 52524 MW; 5BB3914F6741AE10 CRC64;

Query Match 69.7%; Score 1840.5; DB 10; Length 495;
Best Local Similarity 75.6%; Pred. No. 1e-122;
Matches 357; Conservative 38; Mismatches 64; Indels 13; Gaps 5;

QY 8 AEQLAQLGPNNTDASAAALICGHFAAVDSKFDVDTAFVADNTYLLFSAYLVFVSMOLGFA 67
Db 5 ADTLGLPLIG---TAAANATDYLNCQFA-----DTTSAVDSTYLLFSAYLVFVSMOLGFA 54
QY 68 MLCAGSVRAKNTMIMLTNVLDAAGGLFYLLFGFAFGSPNGFTGKHFFGLKDIPSS 127
Db 55 MLCAGSVRAKNTMIMLTNVLDAAGGLFYLLFGFAFGAFAPNGSNGFTGKHFFGLKQVQV 114
QY 128 SYDYSFLYQWAFIAAAGITSGSIABRTQFVAYLIYSSELTGFVYVPSVHFWSPDQWA 187
Db 115 GFDYSFPLFQWAFIAAAGITSGSIABRTQFVAYLIYSSELTGFVYVPSVHFWSPDQWA 174
QY 168 SAFKIT-DRLFSTGVDFAGSVVHVGGLTAGLWGLALIEGPRGRDHAGRAVALRGHSA 246
Db 175 SASRTSGSLFGSGVIDFAGSVVHVAACRTL-GRPHRGPPHWRFDHAGRSVALRGHSA 233
QY 247 SLVVLGTLLFGWNGFNPSPFNKILLTYGNSGNYGOWSAVGRVAVTTTLAGSTAAALT 306

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Db 234 SLVVLGSFLLFWGNGFNPSPFTILKSYGPPSGTHGOWSAVGRVAVTTTLAGSTAAALT 293
QY 307 LFKRVISGHNVNVDVCGNLGGFAATAGCGSVVEPMAIIVCGFVASIVLIACNKLAEKV 366
Db 294 LFKRLQTHNVNVDVCGNLGGFAATAGCGSVVDPMAIICGVFSAWLIGLNAALRL 353
QY 367 KFDPLLEAAQLHGGCGTGWVIFTALFAKKEVYKVEYGL-GRAGLMLGGGKLLAAHVQ 425
Db 354 KFDPLLEAAQLHGGCGAGVIFTALFAKKEVYDQIFGQPRPYGLFMGGGRLGAIHW 413
QY 426 ILVIAGVSTAGTGLFWGLNKLKLRISSDELACMDMTRHGGFAYAYEDDE 477
Db 414 ILVIAAWSFMTAPLFLVLNKLGLLRISAEDEMAGMDQTRHGGFAYAYHDDD 465

RESULT 9
ID O04400 PRELIMINARY; PRT; 533 AA.
AC O04400;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative ammonium transporter OsAMT1p.
GN OSAMT1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Nimmann O., Jauniaux J.C., Frommer W.B.;
RT "Identification of a high affinity NH4+ transporter from plants.";
RL EMBL J. 13:3464-3471(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=Nipponbare; TISSUE=Root;
RC von Wiren N., Bergfeld A., Nimmann O., Frommer W.B.;
RT "OsAMT1-1, a putative ammonium transporter cDNA from rice.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001505; AAB58937.1; -.
DR PIR; T03441; T03441.
DR Gramene; O04400; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0008519; P:ammonium transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium transp.
DR Pfam; PF00909; Ammonium transp; 1.
DR TIGRFAMs; TIGR00836; amt; 1.
DR PROSITE; PS01219; AMMONIUM TRANSP; 1.
SQ SEQUENCE 533 AA; 56943 MW; AA06F72D188A0E44 CRC64;

Query Match 67.9%; Score 1792.5; DB 10; Length 533;
Best Local Similarity 71.6%; Pred. No. 2.9e-119;
Matches 361; Conservative 39; Mismatches 77; Indels 27; Gaps 11;

QY 3 LPACBAQLGPNNTDASAAALICGHFAAVDSKFDVDTAFVADNTYLLFSAYLVFVSM 62
Db 1 MATCAAD-LAPLIGP---VAANATDYLNCRFA-----DTTSAVDATYLLFSAYLVFAM 49
QY 63 QLGFAMLCAGSVRAKNTMIMLTNVLDAAGGLFYLLFGFAF---AFGPSNGFTGKHFF 119
Db 50 QLGFAMLCAGSVRAKNTMIMLTNVLDAAGGLFYLLFGFASLRDLRTPSNGFTGKHFF 109
QY 120 GLKDIPS-SSYDYSFLYQWAFIAAAGITSGSIABRTQFVAYLIYSSELTGFVYVPSVH 178
Db 110 GLKHPARPSDDVDFLQWAFIAAAGITSGSIABRTQFVAYLIYSSELTGFVYVPSVH 169
QY 179 WFWSPDQWASAFKIT-DRLFSTGVDFAGSVVHVGGLTAGLWGLALIEGPRGRDHAGR 237
Db 170 WINSADGWASASRTSGPLFGSGVIDFAGSVVHVGGLTAGLWGLALIEGPRGRDHAGR 229

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238 AVALRGHSASLVLTGFTLLWFGWYGNPGSFNKKILLTYGNSGNYGQMSAVGRTAVTTTL 297
 239 SVALRGHSASLVLTGFTLLWFGWYGNPGSFNKKILLTYGNSGNYGQMSAVGRTAVTTTL 289
 298 AGSTAATLTTLFGKRVISGHNVTDVNCGLLGGGFAATAGCSVVBPWAAIVCGFVASIVLI 357
 299 AGSVAATLTTLFGKRVISGHNVTDVNCGLLGGGFAATAGCSVVBPWAAIVCGFVASIVLI 349
 358 ACKNLAKEVKFDDPLEAAQLHGCGGTWGIPTALFAKKEVYKVEVYGLGRAGLLMGGGK 417
 359 GLN-LAARLAFDDPLEAAQLHGCGGTWGIPTALFAKKEVYKVEVYGLGRAGLLMGGGK 406
 418 LLAHVITQILVIAAGWSATMPLFWLGNKLLRISSEDELAGMDTRHGGFAYAYEDE 477
 407 LLGAVITQILVIAAGWSATMPLFWLGNKLLRISSEDELAGMDTRHGGFAYAYEDE 466
 478 THKH----GNQLR----RVCPNAS 493
 467 EHKSGVGGFMRLRSQAOTRVEFAAA 490

RESULT 10

Q947NO PRELIMINARY; PRT; 497 AA.
 AC Q947NO;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Ammonium transporter 1-2.
 GN OSAMTI-2.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 NCBI_TaxID=4530;
 [1]
 SEQUENCE FROM N.A.
 RA Horne M.S., Masle J., Udvardi M.K., Upadhyaya N.M.;
 RT "Cloning and characterization of three Ammonium transporter genes from rice."
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF289478; AAL05613.1; -
 DR Gramene; Q947NO; -
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008519; F:ammonium transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001905; Ammonium_transpt.
 DR Pfam; PF00909; Ammonium_transp; 1.
 DR TIGRFAMs; TIGR00836; amt; 1.
 DR PROSITE; PS01219; AMMONIUM_TRANS; 1.
 FT NON TER 1
 FT NON TER 335
 SQ SEQUENCE 497 AA; 53398 MW; 8A054402C44C3D24 CRC64;

Query Match 62.7%; Score 1655.5; DB 10; Length 497;
 Best Local Similarity 65.6%; Pred. No. 1.4e-109;
 Matches 330; Conservative 53; Mismatches 81; Indels 39; Gaps 9;
 9 BOLAQLIG--PNTVDASAAASLICGHPAAVDSKFDVDTAFADNTYLLFSAYLVFSNQLGF 66
 6 DSLGPLLGGANSTD--AANYIC-----NRFDTSSAVDATYLLFSAYLVFAMQLGF 55
 67 AMLCAGSVRAKNTNIMLTNVDAAAGLFPYLLFGAPAFGPSNPGFKHFFGLKDIPS 126
 56 AMLCAGSVRAKNSVNTNVDAAAGLFPYLLFGA--SRRTPSKGFQKQFFGLKHPQ 114
 127 SSYDYSFLYQWAFIAAAGITSGSIAERTQFVAYLIYSFSLTGFVYVSVHFWSPDGM 186
 115 TGYDYDFLFWAFIAAAGITSGSIAERTQFVAYLIYSFSLTGFVYVSVHFWSTDCM 174
 187 ASAFKIT--DRLFSTGVDFAGSGVHVMVGGIAGLWGLIEGPMGRFDHAGRAVALRGHS 245
 175 ASAGRLTGFLLFKSGVIDFAGSGVHVMVGGIAGLWGLIEGPMGRFDHAGRAVALRGHS 234

246 ASLVLTGFTLLWFGWYGNPGSFNKKILLTYGNSGNYGQMSAVGRTAVTTTL 305
 235 ASLVLTGFTLLWFGWYGNPGSFNKKILLTYGNSGNYGQMSAVGRTAVTTTL 293
 306 TLFGRKRVISGHNVTDVNCGLL-----GGFAAITAGCSVVBPWAAIVCGFVASIV 355
 294 -----NHAVROEMADGALERDRRLQSPRRVRAITAGCSVVDPWASVCGFVSANW 344
 356 LIACKNLAKEVKFDDPLEAAQLHGCGGTWGIPTALFAKKEVYKVEVYGL-GRAGLLMG 414
 345 LIGCNKLLALMKFDDPLEATQLHGCGGAWGIIPTALFAKKEVYKVEVYGLVGPGRPYGLFM 404
 415 GKKLLAAHVITQILVIAAGWSATMPLFWLGNKLLRISSEDELAGMDTRHGGFAYAYE 474
 405 GGRLLAAHVITQILVIAAGWSATMPLFWLGNKLLRISSEDELAGMDTRHGGFAYAYE 464
 475 DBETH----KHGMQLRRVGPNAS 493
 465 DEGQRRVRAKSAETARVEPRKS 487

RESULT 11

Q9ZPM8 PRELIMINARY; PRT; 335 AA.
 AC Q9ZPM8;
 DT 01-MAY-1999 (TREMELrel. 10, Created)
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)
 DE Ammonium transporter (Fragment).
 GN AMT1.
 OS Nepenthes alata (Winged pitcher plant).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Nepenthaceae; Nepenthes.
 NCBI_TaxID=4376;
 [1]
 SEQUENCE FROM N.A.
 RA TISSUE=Pitcher;
 RA Schulte W., Frommer W.B., Ward J.M.;
 RT "Transporters for ammonium, amino acids and peptides are expressed in pitchers of the carnivorous plant Nepenthes."
 RL Plant J. 17:1101-110(1999).
 DR EMBL; AF080541; AAD16012.1; -
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0008519; F:ammonium transporter activity; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR001905; Ammonium_transpt.
 DR Pfam; PF00909; Ammonium_transp; 1.
 DR TIGRFAMs; TIGR00836; amt; 1.
 DR PROSITE; PS01219; AMMONIUM_TRANS; 1.
 FT NON TER 1
 FT NON TER 335
 SQ SEQUENCE 335 AA; 35653 MW; 752FDSDFEB75E9F CRC64;

Query Match 55.4%; Score 1463; DB 10; Length 335;
 Best Local Similarity 81.2%; Pred. No. 4.3e-96;
 Matches 272; Conservative 27; Mismatches 33; Indels 2; Gaps 1;
 136 YQWAFIAAAGITSGSIAERTQFVAYLIYSFSLTGFVYVSVHFWSPDGWASAFKIDR 195
 1 YQWAFIAAAGITSGSIAERTQFVAYLIYSFSLTGFVYVSVHFWSPDGWASASRNL 60
 196 LFTGTVIDFAGSGVHVMVGGIAGLWGLIEGPMGRFDHAGRAVALRGHSASLVLTGFL 255
 61 LLGSGVTDVDFAGSGVHVMVGGIAGLWGLIEGPMGRFDHAGRAVALRGHSASLVLTGFL 120
 256 LFWGTGFPNPGSFNKKILLTYGNSGNYGQMSAVGRTAVTTTL 315
 121 LFWGTGFPNPGSFNKKILLTYGNSGNYGQMSAVGRTAVTTTL 180
 316 HNVTDVNCGLLGGFAAITAGCSVVBPWAAIVCGFVASIVLIACNKLAEKVFDDPLEA 375
 181 HNVTDVNCGLLGGFAAITAGCSVVBPWAAIVCGFVASIVLIACNKLAEKVFDDPLEA 240


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30 QY 439 PLFWGLNKLKLLRISSEDELAGMDMTRH 466
31 DB 482 SFFILNKAGLLRVLPLOEMAGLDAANY 509

RESULT 15
Q8LJU0 PRELIMINARY; PRT; 542 AA.
AC Q8LJU0;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Putative ammonium transporter.
OS Chlamydomonas reinhardtii.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
SEQUENCE FROM N.A.
RA Gonzalez-Ballester D., Perez-Alegre M., Fernandez E.;
RT "A putative ammonium transporter (CrAMT1-1) from Chlamydomonas
reinhartii.";
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR Gonzalez-Ballester D., Fernandez E.;
DR "A putative ammonium transporter cDNA of Chlamydomonas reinhardtii.";
DR Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY058211; AAL3852.1; -.
DR GO; GO:0008519; F:ammonium transporter activity; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR001905; Ammonium transp.
DR Pfam; PF00909; Ammonium transp.
DR TIGRFAMs; TIGR00836; amt; 1.
DR PROSITE; PS01219; AMMONIUM TRANSP; 1.
SQ SEQUENCE 539 AA; 57147 MW; 8281E2BBA3B1DD2 CRC64;

Query Match 40.8%; Score 1078; DB 10; Length 539;
Best Local Similarity 43.9%; Pred. No. 1.8e-68;
Matches 223; Conservative 68; Mismatches 165; Indels 52; Gaps 8;

QY 3 LPACPAQLAQLGPNNTDASAAA-----SLICGHFAAVDSFVDTA 44
DB 10 LGSCSVETVALLGYGLEODSITALCQPEGAGCTSTDCNCFQYLMGATADASTADVG 69
QY 45 FAVNTVLLFSAYLVFSMQLGFAVLCAAGSRAKNTNMIMTLNVLDAAAGGLFYFLGFAF 104
DB 70 VGLDVSPFLFSGYLVFMQLGFAVLCAAGSRAKNTNMIMTLNVLDAAAGGLFYFLGFAF 129
QY 105 A-----FGSPNGFIGKHFFGLKDIPISS-----YDYSFLYQWAFIAAAGITSGSI 152
DB 130 AYGRKYQNSNGFTGNWNFALSYYTTSMTSGTFTTGFQWHPFFQWSPCAATTIVSGAV 189
QY 153 AERTQFVAYLISSELTGFVYVWVSHWSPDQWASAFKITDRLFTSTGVDFPAGSGVWVHV 208
DB 190 AERTFVAYLISSELTGFVYVWVSHWSPDQWASAFKITDRLFTSTGVDFPAGSGVWVHV 249
QY 209 VYHVGGLAGLIEGPRMGRPDHAGRAVALRHSASLVLTGTFLLWFGWYGNPFGSKILL 268
DB 250 VYHVGGLAGLIEGPRMGRPDHAGRAVALRHSASLVLTGTFLLWFGWYGNPFGSKILL 308
QY 269 NKILLTYGNSNYGQWASVGRVAVTTLAGSTAALTTLTGKRVISGH--NNVTDVCGNLLGGF 328
DB 309 NKILLTYGNSNYGQWASVGRVAVTTLAGSTAALTTLTGKRVISGH--NNVTDVCGNLLGGF 361
QY 329 GFAAITAGCSVVEPWAIVCGFVASIVLIACNKLAEKVKFDDPLEAAQLHGGCGTGWVIFTA 387
DB 362 GLVAVTASCSVIEPWAIVCGFVASIVLIACNKLAEKVKFDDPLEAAQLHGGCGTGWVIFTA 421
QY 388 FTALFAKKEVYKVEYGL-----GRAHLLMGCGGKLLAAHVLIQIIVIAVGSATWG 438
DB 422 FPGFLAAPHYVVEYVYAGFGMDAREGRFLGYGGHGVLLVOLLIEVLAIFGWTGFMWG 481

Query Match 36.7%; Score 968; DB 10; Length 542;
Best Local Similarity 42.6%; Pred. No. 1.2e-60;
Matches 222; Conservative 66; Mismatches 165; Indels 68; Gaps 14;

QY 5 ACPEAQLAQLGPNNTDASAAALICGHFAA-----VD-----SKFVD----- 42
DB 4 ACILAAKSALVG--VANGDSLASATCAAMEAAAPVARHLQETTVDTLTLOETVDTIGLNL 61
QY 43 --TAFVAVNTVLLFSAYLVFSMQLGFAVLCAAGSRAKNTNMIMTLNVLDAAAGGLFYFLF 100
DB 62 QGTMDGLNTLLLYLGGALVFLMHGGSAMLEAGRSKANNILLQTVLDASCSALMWYFV 121
QY 101 GFAPAF--GSPNGFIGKHFFGLKDIPISS-----SSSYDYSFLYQWAFIAAAGITSGSIA 153
DB 122 GFAPAFGIGDKPKNTIGNAFALVDIDTHTGSGTGKWDWFFQWAFATAATVTPAGAVA 181
QY 154 ERTQFVAYLISSELTGFVYVWVSHWSPDQWASAFKITDRLFTSTGVDFPAGSGVWVHV 213
DB 182 ERTFVAYLISSELTGFVYVWVSHWSPDQWASAFKITDRLFTSTGVDFPAGSGVWVHV 240
QY 214 GGIAGLWGLALIEGPRMGRPDHAGRAVALRHSASLVLTGTFLLWFGWYGNPFGSKILL 273
DB 241 GGLAGLIGAIMVDPRLGRPDADGKPDVMPGHSAIILVLTGTVLLWFGWYGNPFGSKILL 297
QY 274 TYGNSNYGQWASVGRVAVTTLAGSTAALTTLTGKRVISGH--NNVTDVCGNLLGGF 330
DB 298 I--NSSTYA---IVCGRAAVCTTLTLAGAAGGVSCLIFG---FARHGRWDLVLCNGLICGP 349
QY 331 AAITAGCSVVEPWAIVCGFVASIVLIACNKLAEKVKFDDPLEAAQLHGGCGTGWVIFTA 390
DB 350 VAVTACPHVYVVEPWAIVCGFVASIVLIACNKLAEKVKFDDPLEAAQLHGGCGTGWVIFTA 409
QY 391 LFAKKEVYKVEYGL-----RAHLLMGCGGKLLAAHVLIQIIVIA 430
DB 410 LFAKKEVYKVEYGL-----RAHLLMGCGGKLLAAHVLIQIIVIA 469
QY 431 GWYSATWGFLFWGLNKLKLLRISSEDELAGMDMTRHGGFAY 471
DB 470 GWYIGNMVFFGIFQFPFGALRIPPEEEMGLDRSKHGGSA 510
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Search completed: March 9, 2004, 11:55:36
Job time : 50 secs
